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OM protein - protein search, using sw model

Run on: April 16, 2005, 03:28:04 ; Search time 136 Seconds

(Without alignments)

674.517 Million cell updates/sec

Title: US-10-753-079-1

Perfect score: 1528

Sequence: 1 DSEDESHITITDELPLK.....RRKKQRVKIAYEISIFVKQM 276

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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20:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1528	100.0	276	9	US-09-766-778-1
2	1528	100.0	276	13	US-10-086-176A-5
3	1528	100.0	276	14	US-10-270-478-1
4	1528	100.0	276	14	US-10-270-479-1
5	1528	100.0	276	16	US-10-753-079-1
6	1528	100.0	276	17	US-10-753-078A-1
7	1528	100.0	277	14	US-10-270-478-2
8	1528	100.0	277	14	US-10-270-479-2
9	1528	100.0	304	14	US-10-167-351-1
10	1528	100.0	304	16	US-10-755-889-412
11	1528	100.0	352	17	US-10-860-277-2
12	1525	99.8	276	9	US-09-741-106-9
13	1525	99.8	276	17	US-10-918-366-9
					Sequence 1, Appli
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					Sequence 1, Appli
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					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 412, App
					Sequence 2, Appli
					Sequence 9, Appli

14	1525	99.8	276	17	US-10-860-277-3	Sequence 3, Appli
15	1522	99.6	304	14	US-10-377-817-2	Sequence 2, Appli
16	1447.5	94.7	291	10	US-09-992-600A-48	Sequence 48, Appli
17	1447.5	94.7	291	10	US-09-924-340-48	Sequence 48, Appli
18	1447.5	94.7	291	10	US-09-992-095B-48	Sequence 48, Appli
19	1447.5	94.7	291	10	US-09-999-570-48	Sequence 48, Appli
20	1447.5	94.7	291	14	US-10-000-489-48	Sequence 48, Appli
21	1447.5	94.7	291	14	US-10-000-986-48	Sequence 48, Appli
22	1447.5	94.7	291	14	US-10-154-678-48	Sequence 48, Appli
23	1447.5	94.7	291	17	US-10-838-854-48	Sequence 48, Appli
24	1444.5	94.5	291	10	US-09-992-600A-52	Sequence 52, Appli
25	1444.5	94.5	291	10	US-09-924-340-52	Sequence 52, Appli
26	1444.5	94.5	291	10	US-09-992-095B-52	Sequence 52, Appli
27	1444.5	94.5	291	10	US-09-999-570-52	Sequence 52, Appli
28	1444.5	94.5	291	14	US-10-000-489-52	Sequence 52, Appli
29	1444.5	94.5	291	14	US-10-000-986-52	Sequence 52, Appli
30	1444.5	94.5	291	14	US-10-154-678-52	Sequence 52, Appli
31	1444.5	94.5	291	17	US-10-838-854-52	Sequence 52, Appli
32	901	59.0	160	15	US-10-408-166-472	Sequence 472, App
33	897	58.7	161	9	US-09-741-106-19	Sequence 19, Appli
34	897	58.7	161	17	US-10-918-366-19	Sequence 19, Appli
35	745	48.8	164	10	US-09-992-600A-96	Sequence 96, Appli
36	745	48.8	164	10	US-09-924-340-96	Sequence 96, Appli
37	745	48.8	164	10	US-09-992-095B-96	Sequence 96, Appli
38	745	48.8	164	10	US-09-999-570-96	Sequence 96, Appli
39	745	48.8	164	14	US-10-000-489-96	Sequence 96, Appli
40	745	48.8	164	14	US-10-000-986-96	Sequence 96, Appli
41	745	48.8	164	14	US-10-154-678-96	Sequence 96, Appli
42	745	48.8	164	17	US-10-838-854-96	Sequence 96, Appli
43	660	43.2	152	10	US-09-992-600A-94	Sequence 94, Appli
44	660	43.2	152	10	US-09-924-340-94	Sequence 94, Appli
45	660	43.2	152	10	US-09-992-095B-94	Sequence 94, Appli

#### ALIGNMENTS

RESULT 1

US-09-766-778-1

; Sequence 1, Application US/09766778

; Patent No. US20010018204A1

; GENERAL INFORMATION:

; APPLICANT: Papathanassiou, Adonia E

; Green, Shawn J.

; TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jones & Askew

; STREET: 191 Peachtree Street, 37th Floor

; City: Atlanta

; STATE: Georgia

; COUNTRY: U.S.A.

; ZIP: 30303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/766,778

; FILING DATE: 22-Jan-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/227,955

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Greene, Jamie L.

; REGISTRATION NUMBER: 32,467

; REFERENCE/DOCKET NUMBER: 05213-0290

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404) 818-3700

; TELEFAX: (404) 818-3799

```
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 276 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: Active-site
/ LOCATION: 2..3
/ OTHER INFORMATION: /note= "Site of partial
/ phosphorylation"
/ FEATURE:
/ NAME/KEY: Active-site
/ LOCATION: 117..118
/ OTHER INFORMATION: /note= "Potential site for N-linked
/ glycosylation"
/ FEATURE:
/ NAME/KEY: Active-site
/ LOCATION: 167..168
/ OTHER INFORMATION: /note= "Potential site for N-linked
/ glycosylation"
/ FEATURE:
/ NAME/KEY: Active-site
/ LOCATION: 228..229
/ OTHER INFORMATION: /note= "Potential site for N-linked
/ glycosylation"
/ FEATURE:
/ NAME/KEY: Domain
/ LOCATION: 26..76
/ OTHER INFORMATION: /label= Kunitz-1
/ FEATURE:
/ NAME/KEY: Domain
/ LOCATION: 97..147
/ OTHER INFORMATION: /label= Kunitz-2
/ FEATURE:
/ NAME/KEY: Domain
/ LOCATION: 189..239
/ OTHER INFORMATION: /label= Kunitz-3
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-766-778-1

Query Match 100.0%; Score 1528; DB 9; Length 276;
Best Local Similarity 100.0%; Pred. No. 6.6e-137;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTIITDTELPPLKLMHSFCFAKADGPGCKAIMEKFFNFITRQCEEFYGGCE 60
Db 1 DSEDEEHTIITDTELPPLKLMHSFCFAKADGPGCKAIMEKFFNFITRQCEEFYGGCE 60
Qy 61 GNQRFESLEECKKMCCTRDNANRIIKTTLOEKDPDFCFLEEDPGICRGYITRYFNNQTK 120
Db 61 GNQRFESLEECKKMCCTRDNANRIIKTTLOEKDPDFCFLEEDPGICRGYITRYFNNQTK 120
Qy 121 QCFERFKYGGCLGNMNNFETLEECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVP 180
Db 121 QCFERFKYGGCLGNMNNFETLEECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVP 180
Qy 181 FEFHGPSWCLTPADRGICRANENRFFYNSVIGKCRPFKYSGCCGNENNFTSKQECRLACK 240
Db 181 FEFHGPSWCLTPADRGICRANENRFFYNSVIGKCRPFKYSGCCGNENNFTSKQECRLACK 240
Qy 241 KGFIQRISKGGLIKTKRKRKQKVIAEYEIFVKNM 276
Db 241 KGFIQRISKGGLIKTKRKRKQKVIAEYEIFVKNM 276

RESULT 2
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US-10-086-176A-5
/ Sequence 5, Application US/10086176A
/ Publication No. US20020173465A1
/ GENERAL INFORMATION:
/ APPLICANT: Hembrough, Todd
/ APPLICANT: Papathanasiou, Adonia E.
/ APPLICANT: Green, Shawn J.
/ TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation Co
/ TITLE OF INVENTION: TFPI Fragments
/ FILE REFERENCE: 05213-0296 43170-266780
/ CURRENT APPLICATION NUMBER: US/10/086.176A
/ CURRENT FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US 09/766,778
/ PRIOR FILING DATE: 2001-01-22
/ PRIOR APPLICATION NUMBER: US 09/227,955
/ PRIOR FILING DATE: 1999-01-11
/ PRIOR APPLICATION NUMBER: US 08/796,850
/ PRIOR FILING DATE: 1997-02-06
/ PRIOR APPLICATION NUMBER: US 09/130,273
/ PRIOR FILING DATE: 1998-08-06
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 5
/ LENGTH: 276
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
US-10-086-176A-5

Query Match 100.0%; Score 1528; DB 13; Length 276;
Best Local Similarity 100.0%; Pred. No. 6.6e-137;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTIITDTELPPLKLMHSFCFAKADGPGCKAIMEKFFNFITRQCEEFYGGCE 60
Db 1 DSEDEEHTIITDTELPPLKLMHSFCFAKADGPGCKAIMEKFFNFITRQCEEFYGGCE 60
Qy 61 GNQRFESLEECKKMCCTRDNANRIIKTTLOEKDPDFCFLEEDPGICRGYITRYFNNQTK 120
Db 61 GNQRFESLEECKKMCCTRDNANRIIKTTLOEKDPDFCFLEEDPGICRGYITRYFNNQTK 120
Qy 121 QCFERFKYGGCLGNMNNFETLEECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVP 180
Db 121 QCFERFKYGGCLGNMNNFETLEECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVP 180
Qy 181 FEFHGPSWCLTPADRGICRANENRFFYNSVIGKCRPFKYSGCCGNENNFTSKQECRLACK 240
Db 181 FEFHGPSWCLTPADRGICRANENRFFYNSVIGKCRPFKYSGCCGNENNFTSKQECRLACK 240
Qy 241 KGFIQRISKGGLIKTKRKRKQKVIAEYEIFVKNM 276
Db 241 KGFIQRISKGGLIKTKRKRKQKVIAEYEIFVKNM 276

RESULT 3
US-10-270-478-1
/ Sequence 1, Application US/10270478
/ Publication No. US20030139339A1
/ GENERAL INFORMATION:
/ APPLICANT: Creasey, Abba
/ TITLE OF INVENTION: Treatment of Severe Pneumonia by
/ TITLE OF INVENTION: Administration of Tissue Factor Pathway Inhibitor (TFPI)
/ FILE REFERENCE: 012441.00027
/ CURRENT APPLICATION NUMBER: US/10/270,478
/ CURRENT FILING DATE: 2002-10-15
/ PRIOR APPLICATION NUMBER: US 60/328,806
/ PRIOR FILING DATE: 2001-10-15
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 276
/ TYPE: PRT
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; PRIOR APPLICATION NUMBER: US 60/509,277
; PRIOR FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US 60/512,199
; PRIOR FILING DATE: 2003-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-753-078A-1

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Best Local Similarity 100.0%; Pred. No. 6.6e-137;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTELPPLKLMHSFCAKADGPGCKAIMKRFNFITRQCEEFYGGCE 60
DB 1 DSEDEEHTIITDTELPPLKLMHSFCAKADGPGCKAIMKRFNFITRQCEEFYGGCE 60
QY 61 GQNRPFESLECKKMCCTRDNANRIIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNOTK 120
DB 61 GQNRPFESLECKKMCCTRDNANRIIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNOTK 120
QY 121 QCFERFYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVP 180
DB 121 QCFERFYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVP 180
QY 181 FEHGPSWCLTPADRGGLCRANENRFYNSVIGKCRPFKYSGCCGNNFTSKQECRLACK 240
DB 181 FEHGPSWCLTPADRGGLCRANENRFYNSVIGKCRPFKYSGCCGNNFTSKQECRLACK 240
QY 241 KGFQIRISKGGLIKTKRKRKQKQKVIAEIEIFVKNM 276
DB 241 KGFQIRISKGGLIKTKRKRKQKQKVIAEIEIFVKNM 276

RESULT 7
US-10-270-478-2
; Sequence 2, Application US/10270478
; Publication No. US2003013939A1
; GENERAL INFORMATION:
; APPLICANT: Creasey, Abba
; TITLE OF INVENTION: Treatment of Severe Pneumonia by
; TITLE OF INVENTION: Administration of Tissue Factor Pathway Inhibitor (TFPI)
; FILE REFERENCE: 012441.00027
; CURRENT APPLICATION NUMBER: US/10/270,478
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/328,806
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-270-478-2

Query Match      100.0%; Score 1528; DB 14; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.7e-137;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTELPPLKLMHSFCAKADGPGCKAIMKRFNFITRQCEEFYGGCE 60
DB 2 DSEDEEHTIITDTELPPLKLMHSFCAKADGPGCKAIMKRFNFITRQCEEFYGGCE 61
QY 61 GQNRPFESLECKKMCCTRDNANRIIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNOTK 120
DB 62 GQNRPFESLECKKMCCTRDNANRIIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNOTK 121
QY 121 QCFERFYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVP 180
DB 122 QCFERFYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVP 181
QY 181 FEHGPSWCLTPADRGGLCRANENRFYNSVIGKCRPFKYSGCCGNNFTSKQECRLACK 240
DB 182 FEHGPSWCLTPADRGGLCRANENRFYNSVIGKCRPFKYSGCCGNNFTSKQECRLACK 241
QY 241 KGFQIRISKGGLIKTKRKRKQKQKVIAEIEIFVKNM 276
DB 242 KGFQIRISKGGLIKTKRKRKQKQKVIAEIEIFVKNM 277

RESULT 8
US-10-270-479-2
; Sequence 2, Application US/10270479
; Publication No. US20030139340A1
; GENERAL INFORMATION:
; APPLICANT: Creasey, Abba
; TITLE OF INVENTION: Treatment of Sepsis By Low-Dose
; TITLE OF INVENTION: Administration of Tissue Factor Pathway Inhibitor (TFPI)
; FILE REFERENCE: 012441.00026
; CURRENT APPLICATION NUMBER: US/10/270,479
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/328,806
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-270-479-2

Query Match      100.0%; Score 1528; DB 14; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.7e-137;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTELPPLKLMHSFCAKADGPGCKAIMKRFNFITRQCEEFYGGCE 60
DB 2 DSEDEEHTIITDTELPPLKLMHSFCAKADGPGCKAIMKRFNFITRQCEEFYGGCE 61
QY 61 GQNRPFESLECKKMCCTRDNANRIIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNOTK 120
DB 62 GQNRPFESLECKKMCCTRDNANRIIKTTLQOEKPDFCFLEEDPGICRGYITRYFYNNOTK 121
QY 121 QCFERFYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVP 180
DB 122 QCFERFYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVP 181
QY 181 FEHGPSWCLTPADRGGLCRANENRFYNSVIGKCRPFKYSGCCGNNFTSKQECRLACK 240
DB 182 FEHGPSWCLTPADRGGLCRANENRFYNSVIGKCRPFKYSGCCGNNFTSKQECRLACK 241
QY 241 KGFQIRISKGGLIKTKRKRKQKQKVIAEIEIFVKNM 276
DB 242 KGFQIRISKGGLIKTKRKRKQKQKVIAEIEIFVKNM 277

RESULT 9
US-10-167-351-1
; Sequence 1, Application US/10167351
; Publication No. US20030165896A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Markland, William
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains
; FILE REFERENCE: DXX-007.2P US-4
; CURRENT APPLICATION NUMBER: US/10/167,351
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 09/638,770
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 09/414,878
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: 09/240,136
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; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 08/676,124
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: PCT/US95/00298
; PRIOR FILING DATE: 1995-01-11
; PRIOR APPLICATION NUMBER: 08/208,265
; PRIOR FILING DATE: 1994-03-10
; PRIOR APPLICATION NUMBER: 08/179,658
; PRIOR FILING DATE: 1994-01-11
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-167-351-1

Query Match          100.0%; Score 1528; DB 14; Length 304;
Best Local Similarity 100.0%; Pred. No. 7.5e-137;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTIITDELPLPLKMHSCAFKADGGPCAKIMKFFNFIFRQCEEFYGGCE 60
Db 29 DSEDEEHTIITDELPLPLKMHSCAFKADGGPCAKIMKFFNFIFRQCEEFYGGCE 88

Qy 61 GQNRFSLECKKCMCTRDNANRIKTTLOQEKDFCFLEEDPGICRGYITRYFYNNQTK 120
Db 89 GQNRFSLECKKCMCTRDNANRIKTTLOQEKDFCFLEEDPGICRGYITRYFYNNQTK 148

Qy 121 QCERFKYGGCLGNMNFETLECKNICEDGPNQFQVNDYGTQLNAVNNSLTPQSTKVPSL 180
Db 149 QCERFKYGGCLGNMNFETLECKNICEDGPNQFQVNDYGTQLNAVNNSLTPQSTKVPSL 208

Qy 181 FEHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 240
Db 209 FEHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 268

Qy 241 KGFTORISKGLIKTKRKRKQKVIAVEEIFVKNM 276
Db 269 KGFTORISKGLIKTKRKRKQKVIAVEEIFVKNM 304

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 412
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-412
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Query Match          100.0%; Score 1528; DB 16; Length 304;
Best Local Similarity 100.0%; Pred. No. 7.5e-137;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 29 DSEDEEHTIITDELPLPLKMHSCAFKADGGPCAKIMKFFNFIFRQCEEFYGGCE 88
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Db 89 GQNRFSLECKKCMCTRDNANRIKTTLOQEKDFCFLEEDPGICRGYITRYFYNNQTK 148

Qy 121 QCERFKYGGCLGNMNFETLECKNICEDGPNQFQVNDYGTQLNAVNNSLTPQSTKVPSL 180
Db 149 QCERFKYGGCLGNMNFETLECKNICEDGPNQFQVNDYGTQLNAVNNSLTPQSTKVPSL 208

Qy 181 FEHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 240
Db 209 FEHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 268

Qy 241 KGFTORISKGLIKTKRKRKQKVIAVEEIFVKNM 276
Db 269 KGFTORISKGLIKTKRKRKQKVIAVEEIFVKNM 304

; TITLE OF INVENTION: Production of Tissue Factor Pathway
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/860,277
; FILING DATE: 04-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/639,273
; FILING DATE: 15-Aug-2000
; APPLICATION NUMBER: US/08/286,530
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Saveriede, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0991.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-860-277-2

Query Match          100.0%; Score 1528; DB 17; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-137;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTIITDELPLPLKMHSCAFKADGGPCAKIMKFFNFIFRQCEEFYGGCE 60
Db 77 DSEDEEHTIITDELPLPLKMHSCAFKADGGPCAKIMKFFNFIFRQCEEFYGGCE 136

Qy 61 GQNRFSLECKKCMCTRDNANRIKTTLOQEKDFCFLEEDPGICRGYITRYFYNNQTK 120
```

Db 137 GQNRFSLECKKCMCTRDNANRIKTTLOQEKDFCFLEEDPGICRGYITRYFNNQTK 196  
 QY 121 QCRPFYGGCLGNMNFETLECKNICEDGPNQFVDNYGTOLNAVNNSLTPQSTKVPSSL 180  
 Db 197 QCRPFYGGCLGNMNFETLECKNICEDGPNQFVDNYGTOLNAVNNSLTPQSTKVPSSL 256  
 QY 181 FEHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFYSGCGGNENFTSKOECLRACK 240  
 Db 257 FEHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFYSGCGGNENFTSKOECLRACK 316  
 QY 241 KGFQIRISGGLIKTKRKKQKRVKIAYEEIFVKM 276  
 Db 317 KGFQIRISGGLIKTKRKKQKRVKIAYEEIFVKM 352

## RESULT 12

US-09-741-106-9  
 ; Sequence 9, Application US/09741106  
 ; Publication No. US20020197667A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Innis, Michael  
 ; Creasey, Abia  
 ; TITLE OF INVENTION: Chimeric Proteins  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Chiron Corporation  
 ; STREET: 4560 Horton St.  
 ; CITY: Emeryville  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94608  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30B  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/741,106  
 ; FILING DATE: 12-Dec-2000  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/286,521  
 ; FILING DATE: 1994-08-05  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saveriede, Paul B.  
 ; REGISTRATION NUMBER: 36,914  
 ; REFERENCE/DOCKET NUMBER: 0990.001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 510-601-2585  
 ; TELEFAX: 510-655-3542  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 276 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Query Match 99.8%; Score 1525; DB 9; Length 276;  
 Best Local Similarity 99.6%; Pred. No. 1.3e-136;  
 Matches 275; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSEDEEHTIITDTELPPLKLMHSFCFAKADGDPCKAIMKRFNFITRQCEFIYGCCE 60  
 Db 1 DSEDEEHTIITDTELPPLKLMHSFCFAKADGDPCKAIMKRFNFITRQCEFIYGCCE 60  
 QY 61 GQNRFSLECKKCMCTRDNANRIKTTLOQEKDFCFLEEDPGICRGYITRYFNNQTK 120  
 Db 61 GQNRFSLECKKCMCTRDNANRIKTTLOQEKDFCFLEEDPGICRGYITRYFNNQTK 120

QY 121 QCRPFYGGCLGNMNFETLECKNICEDGPNQFVDNYGTOLNAVNNSLTPQSTKVPSSL 180  
 Db 121 QCRPFYGGCLGNMNFETLECKNICEDGPNQFVDNYGTOLNAVNNSLTPQSTKVPSSL 180  
 QY 181 FEHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFYSGCGGNENFTSKOECLRACK 240  
 Db 181 FEHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFYSGCGGNENFTSKOECLRACK 240  
 QY 241 KGFQIRISGGLIKTKRKKQKRVKIAYEEIFVKM 276  
 Db 241 KGFQIRISGGLIKTKRKKQKRVKIAYEEIFVKM 276

## RESULT 13

US-10-918-366-9  
 ; Sequence 9, Application US/10918366  
 ; Publication No. US20050008654A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Innis, Michael  
 ; Creasey, Abia  
 ; TITLE OF INVENTION: Chimeric Proteins  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Chiron Corporation  
 ; STREET: 4560 Horton St.  
 ; CITY: Emeryville  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94608  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30B  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/918,366  
 ; FILING DATE: 16-Aug-2004  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/286,521  
 ; FILING DATE: 05-AUG-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saveriede, Paul B.  
 ; REGISTRATION NUMBER: 36,914  
 ; REFERENCE/DOCKET NUMBER: 0990.001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 510-601-2585  
 ; TELEFAX: 510-655-3542  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 276 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Query Match 99.8%; Score 1525; DB 17; Length 276;  
 Best Local Similarity 99.6%; Pred. No. 1.3e-136;  
 Matches 275; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSEDEEHTIITDTELPPLKLMHSFCFAKADGDPCKAIMKRFNFITRQCEFIYGCCE 60  
 Db 1 DSEDEEHTIITDTELPPLKLMHSFCFAKADGDPCKAIMKRFNFITRQCEFIYGCCE 60  
 QY 61 GQNRFSLECKKCMCTRDNANRIKTTLOQEKDFCFLEEDPGICRGYITRYFNNQTK 120  
 Db 61 GQNRFSLECKKCMCTRDNANRIKTTLOQEKDFCFLEEDPGICRGYITRYFNNQTK 120  
 QY 121 QCRPFYGGCLGNMNFETLECKNICEDGPNQFVDNYGTOLNAVNNSLTPQSTKVPSSL 180  
 Db 121 QCRPFYGGCLGNMNFETLECKNICEDGPNQFVDNYGTOLNAVNNSLTPQSTKVPSSL 180

QY 181 FEFGPSCWCLTPADRGCLCRANENRYNSVIGKCRPFKYSGCGNENFTSKQECIRACK 240  
DB 181 FEFGPSCWCLTPADRGCLCRANENRYNSVIGKCRPFKYSGCGNENFTSKQECIRACK 240  
QY 241 KGFIORISKGLIKTKRKRKKQKVIAEIEIFVKNM 276  
DB 241 KGFIORISKGLIKTKRKRKKQKVIAEIEIFVKNM 276

## RESULT 14

US-10-860-277-3  
; Sequence 3, Application US/10860277  
; Publication No. US20050064556A1  
; GENERAL INFORMATION:  
; APPLICANT: Innes, Michael  
; Creasey, Abia  
; TITLE OF INVENTION: Production of Tissue Factor Pathway  
; Inhibitor  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton St.  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/860,277  
; FILING DATE: 15-Aug-2000  
; FILING DATE: 04-Jun-2004  
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/639,273  
; FILING DATE: 15-Aug-2000  
; APPLICATION NUMBER: US/08/286,530  
; FILING DATE: 05-Aug-1994

ATTORNEY/AGENT INFORMATION:  
; NAME: Savereide, Paul B.  
; REGISTRATION NUMBER: 36,914  
; REFERENCE/DOCKET NUMBER: 0991.001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-601-2585  
; TELEFAX: 510-655-3542

INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 276 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-860-277-3

Query Match 99.8%; Score 1525; DB 17; Length 276;  
Best Local Similarity 99.6%; Pred. No. 1.3e-136;  
Matches 275; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTELPPLKLMHSCAFKADGPGCAIMKRPFFNIFTRQCEFIYGCCE 60  
DB 1 DSEDEEHTIITDTELPPLKLMHSCAFKADGPGCAIMKRPFFNIFTRQCEFIYGCCE 60  
QY 61 GQNRPFESLECKKMKCTRDNANRIKTTLOQEKDPFCFLEEDPGICRGYITRYFYNNQTK 120  
DB 61 GQNRPFESLECKKMKCTRDNANRIKTTLOQEKDPFCFLEEDPGICRGYITRYFYNNQTK 120  
QY 121 QCFERFYGGCLGNMNFETLECKNICEDGPNPGFVDNYGTQLNAVNSLTPQSTKVPSL 180  
DB 121 QCFERFYGGCLGNMNFETLECKNICEDGPNPGFVDNYGTQLNAVNSLTPQSTKVPSL 180

QY 181 FEFGPSCWCLTPADRGCLCRANENRYNSVIGKCRPFKYSGCGNENFTSKQECIRACK 240  
DB 181 FEFGPSCWCLTPADRGCLCRANENRYNSVIGKCRPFKYSGCGNENFTSKQECIRACK 240  
QY 241 KGFIORISKGLIKTKRKRKKQKVIAEIEIFVKNM 276  
DB 241 KGFIORISKGLIKTKRKRKKQKVIAEIEIFVKNM 276

## RESULT 15

US-10-377-817-2  
; Sequence 2, Application US/10377817  
; Publication No. US20030166194A1  
; GENERAL INFORMATION:  
; APPLICANT: Broze, George J.  
; Kretzmer, Kuniko K.  
; APPLICANT: Wun, Tze-Chen  
; TITLE OF INVENTION: Antibodies to human tissue factor  
; Inhibitor  
; FILE REFERENCE: SM04941-10-US  
; CURRENT APPLICATION NUMBER: US/10/377,817  
; CURRENT FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: US/09/627,676  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: 09/054,782  
; PRIOR FILING DATE: 1998-04-03  
; PRIOR APPLICATION NUMBER: 08/463,323  
; PRIOR FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: 08/355,351  
; PRIOR FILING DATE: 1993-07-15  
; PRIOR APPLICATION NUMBER: 07/566,280  
; PRIOR FILING DATE: 1990-08-13  
; PRIOR APPLICATION NUMBER: 07/123,753  
; PRIOR FILING DATE: 1987-11-23  
; PRIOR APPLICATION NUMBER: 07/077,366  
; PRIOR FILING DATE: 1987-07-23  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 304  
; TYPE: PRT  
; ORGANISM: human  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(29)  
; OTHER INFORMATION: signal region  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (29)...(304)  
; OTHER INFORMATION: mature protein  
US-10-377-817-2

Query Match 99.6%; Score 1522; DB 14; Length 304;  
Best Local Similarity 99.6%; Pred. No. 2.8e-136;  
Matches 275; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTELPPLKLMHSCAFKADGPGCAIMKRPFFNIFTRQCEFIYGCCE 60  
DB 29 DSEDEEHTIITDTELPPLKLMHSCAFKADGPGCAIMKRPFFNIFTRQCEFIYGCCE 88  
QY 61 GQNRPFESLECKKMKCTRDNANRIKTTLOQEKDPFCFLEEDPGICRGYITRYFYNNQTK 120  
DB 89 GQNRPFESLECKKMKCTRDNANRIKTTLOQEKDPFCFLEEDPGICRGYITRYFYNNQTK 148  
QY 121 QCFERFYGGCLGNMNFETLECKNICEDGPNPGFVDNYGTQLNAVNSLTPQSTKVPSL 180  
DB 149 QCFERFYGGCLGNMNFETLECKNICEDGPNPGFVDNYGTQLNAVNSLTPQSTKVPSL 208  
QY 181 FEFGPSCWCLTPADRGCLCRANENRYNSVIGKCRPFKYSGCGNENFTSKQECIRACK 240  
DB 209 FEFGPSCWCLTPADRGCLCRANENRYNSVIGKCRPFKYSGCGNENFTSKQECIRACK 268

Search completed: April 16, 2005, 03:40:57  
Job time : 138 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2005, 03:15:48 ; Search time 173 Seconds  
(without alignments)  
617.028 Million cell updates/sec

Title: US-10-753-079-1

Perfect score: 1528

Sequence: 1 DSEDEHTITDTLPLK.....PKRKQKVIAIEIFVKNM 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: \_geneseqp1980s:\*
- 2: \_geneseqp1990s:\*
- 3: \_geneseqp2000s:\*
- 4: \_geneseqp2001s:\*
- 5: \_geneseqp2002s:\*
- 6: \_geneseqp2003as:\*
- 7: \_geneseqp2003bs:\*
- 8: \_geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1528	100.0	276	2 AAW30311	Aaw30311 Recombina
2	1528	100.0	276	2 AAW61535	Aaw61535 Human tis
3	1528	100.0	276	6 ABU07724	Abu07724 Human tis
4	1528	100.0	276	7 ADE80824	Ad80824 Human tis
5	1528	100.0	276	7 ADE80822	Ad80822 Human tis
6	1528	100.0	276	7 ADI20097	Adi20097 Human TFP
7	1528	100.0	276	8 ADQ76118	Adq76118 Human tis
8	1528	100.0	276	8 ADQ76119	Adq76119 Human tis
9	1528	100.0	277	7 ADE80825	Ad80825 Human tis
10	1528	100.0	277	7 ADE80823	Ad80823 Human tis
11	1528	100.0	277	7 ADI20098	Adi20098 Human Ala
12	1528	100.0	304	2 AAR67894	Aar67894 Tissue fa
13	1528	100.0	304	2 AAR81884	Aar81884 Lipoprote
14	1528	100.0	304	2 AAY49557	Aay49557 Human lip
15	1528	100.0	304	7 ADF09568	Adf09568 Human tis
16	1528	100.0	304	8 ADG88030	Adg88030 Human ser
17	1528	100.0	304	8 ADR14411	Adr14411 Human NF-
18	1528	100.0	352	2 AAR92011	Aar92011 Ubiquitin
19	1525	99.8	276	2 AAR92012	Aar92012 TFP mute
20	1525	99.8	276	2 AAR92265	Aar92265 TFPI mute
21	1522	99.6	304	3 AAY92002	Aay92002 Human tis
22	1517	99.3	304	1 AAY70273	Aay70273 Human tis
23	1514	99.1	304	2 AAR78389	Aar78389 Human lip
24	1512	98.0	277	2 AAR37312	Aar37312 Non-glyco
25	1507	98.6	304	3 AAY70272	Aay70272 Human mut

26	1502.5	98.3	327	8 ABR83494	Abm83494 Human dia
27	1447.5	94.7	291	6 ABR48476	AbR48476 Human Tif
28	1447	94.7	304	2 AAR42309	Aar42309 LACI gene
29	1446	94.6	265	2 AAR11170	Aar11170 Ser-(Asp1
30	1444.5	94.5	291	6 ABR48478	AbR48478 Human Tif
31	1428.5	93.5	262	2 AAR11172	Aar11172 Ser-(Asp1
32	1422	93.1	261	2 AAR11171	Aar11171 Ser-(Asp1
33	1417	92.7	256	2 AAR11169	Aar11169 Ser-(Asp1-
34	1005	65.8	225	4 AAU02971	Aau02971 Angiotens
35	979.5	64.1	274	8 ABR83495	Abm83495 Human dia
36	934.5	61.2	302	2 AAR35001	Aar35001 LACI, 7/1
37	934.5	61.2	302	2 AAR88513	Aar88513 Lipoprote
38	901	59.0	160	2 AAR23800	Aar23800 LACI frag
39	894	58.5	161	2 AAW00017	Aaw00017 TFPI chim
40	888	58.1	189	2 AAR11167	Aar11167 (Asp1-thr
41	834	54.6	183	2 AAR11146	Aar11146 Ser-(Glu1
42	797	52.2	459	8 ADG74024	Adg74024 Annexin V
43	745	48.8	164	6 ABR48500	AbR48500 Human Tis
44	679	44.4	161	4 AAU02982	Aau02982 Angiotens
45	660	43.2	152	6 ABR48499	AbR48499 Human Tis

## ALIGNMENTS

RESULT 1

AAW30311

ID AAW30311 standard; protein; 276 AA.

XX AC AAW30311;

XX DT 30-JAN-1998 (first entry)

XX DE Recombinant non-glycosylated TFPI.

XX KW Tissue factor pathway inhibitor; TFPI; human; tissue factor inhibitor;

KW Lipoprotein-associated coagulation inhibitor; coagulation inhibitor; TFI;

KW LACI; extrinsic pathway inhibitor; protein refolding; clot-inhibitor;

KW protein solubility modification; EPI.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 2

FT /note= "phosphorylated to varying degrees, but does not

FT affect TFPI function"

FT Disulfide-bond 26..76

FT Disulfide-bond 35..59

FT Disulfide-bond 51..72

FT Disulfide-bond 97..147

FT Disulfide-bond 106..130

FT Disulfide-bond 122..143

FT Disulfide-bond 189..239

FT Disulfide-bond 198..222

FT Disulfide-bond 214..235

XX WO9640784-A2.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US009980.

XX PR 07-JUN-1995; 95US-00473668.

XX PR 07-JUN-1995; 95US-00477677.

XX (CHIR ) CHIRON CORP.

PA (SEAR ) SEARLE & CO G D.

XX Dorin GJ, Arve BH, Pattison GL, Hallenbeck RF, Johnson K, Chen B;

PI Rana RK, Hora MS, Madani H, Gustafson ME, Tsang M, Bild GS;

PI Johnson GV;

XX WPI; 1997-087056/08.

XX Aq. formulation of tissue factor pathway inhibitor - contains charged  
 PT polymer, e.g. dextran sulphate, to facilitate solubilisation, formulation  
 PT purification and refolding of protein.  
 XX Disclosure; Fig 4; 86pp; English.  
 XX This sequence represents the human tissue factor pathway inhibitor (TFPI)  
 CC protein. TFPI is also known as Lipoprotein-associated coagulation  
 CC inhibitor (LACI), extrinsic pathway inhibitor (EPI) and tissue factor  
 CC inhibitor (TFI). The DNA encoding this sequence was altered to contain  
 CC the optimum codons for expression in E. coli, to allow for expression of  
 CC this protein in the bacteria. TFPI is used in the aqueous formulation of  
 CC the invention. The aqueous formulation also includes a charged polymer  
 CC (CP), preferably a sulphated polysaccharide (such as heparin or dextran  
 CC sulphate) or a polyphosphate, preferably immobilised on a solid support.  
 CC The CP is added to aid the correct refolding of TFPI. TFPI can also be  
 CC modified or refolded using the methods of the invention. One method is  
 CC for modifying the solubility of a protein, by adding an aqueous solution  
 CC of a CP to reduce inter- and intra-molecular interactions between the  
 CC charged domains of the protein. The second method is for refolding an  
 CC improperly folded or denatured protein (e.g. TFPI), and comprises adding  
 CC CP to a solution of the protein prior to allowing the protein to refold.  
 CC The methods are particularly useful for solubilising, formulating,  
 CC purifying and refolding proteins (especially TFPI) which have been  
 CC engineered by genetic recombination and produced in bacterial, yeast or  
 CC other cells in a form that has a non-native tertiary structure. TFPI is a  
 CC coagulation inhibitor which has clot-inhibiting properties  
 XX Sequence 276 AA;

Query Match 100.0%; Score 1528; DB 2; Length 276;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-129;  
 Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSEDEEHTIITDTELPPLKLMHSFCADGPKADGPKAKMKRFFNITROCEEFYIGGCE 60  
 Db 1 DSEDEEHTIITDTELPPLKLMHSFCADGPKADGPKAKMKRFFNITROCEEFYIGGCE 60  
 QY 61 GNQRFESLECKKMCCTRDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120  
 Db 61 GNQRFESLECKKMCCTRDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120  
 QY 121 QCERFYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNANVNSLTPOSTKVPSSL 180  
 Db 121 QCERFYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNANVNSLTPOSTKVPSSL 180  
 QY 181 FEHGPSWCLTPADRGICRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECRLACK 240  
 Db 181 FEHGPSWCLTPADRGICRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECRLACK 240  
 QY 241 KGFIQIRISKGLIKTKRKQRVKIAYEIEIFVKNM 276  
 Db 241 KGFIQIRISKGLIKTKRKQRVKIAYEIEIFVKNM 276

## RESULT 2

AAW61535  
 ID AAW61535 standard; protein; 276 AA.  
 AC AAW61535;

DT 06-NOV-1998 (first entry)  
 XX Human tissue factor pathway inhibitor (TFPI).

XX Human tissue factor pathway inhibitor; TFPI; TFPI-2; cell proliferation;  
 KW angiogenesis-related disease; cancer; arthritis; macular degeneration;  
 KW diabetic retinopathy.

XX Homo sapiens.

OS Location/Qualifiers  
 FH Key

FT Modified-site 2  
 FT Domain /note= "Potential phosphorylation site"  
 FT 26..76  
 FT /note= "Kunitz-1 type protease inhibitor domain"  
 FT Disulfide-bond 26..76  
 FT Disulfide-bond 35..59  
 FT Disulfide-bond 51..72  
 FT Domain 97..147  
 FT /note= "Kunitz-2 type protease inhibitor domain"  
 FT Disulfide-bond 97..147  
 FT Disulfide-bond 106..130  
 FT Modified-site 117  
 FT /note= "N-glycosylated"  
 FT Disulfide-bond 122..143  
 FT Modified-site 167  
 FT /note= "N-glycosylated"  
 FT Domain 189..239  
 FT /note= "Kunitz-3 type protease inhibitor domain"  
 FT Disulfide-bond 189..239  
 FT Disulfide-bond 198..222  
 FT Disulfide-bond 214..235  
 FT Modified-site 228  
 FT /note= "N-glycosylated"  
 XX WO9834634-A1.  
 PN 13-AUG-1998.  
 PD 06-FEB-1998; 98WO-US002699.  
 PF 06-FEB-1997; 97US-00796850.  
 PR (ENTR-) ENTREMED INC.  
 PX Papathanassiou AE, Green SJ;  
 PI WPI; 1998-446947/38.  
 DR Composition comprising tissue factor pathway inhibitor for inhibiting  
 PT cell proliferation - for treating angiogenesis related diseases e.g.  
 PT cancer, arthritis, macular degeneration and diabetic retinopathy.  
 XX Claim 6; Page 23-24; 37pp; English.  
 PS The present sequence represents the human tissue factor pathway inhibitor  
 XX (TFPI). The invention provides compositions using TFPI and its homologs,  
 CC e.g. TFPI-2 (AAW61536), for inhibiting cell proliferation. The  
 CC compositions are claimed to be useful for inhibiting an angiogenesis-  
 CC related disease, such as cancer, arthritis, macular degeneration or  
 CC diabetic retinopathy  
 XX Sequence 276 AA;  
 SQ Query Match 100.0%; Score 1528; DB 2; Length 276;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-129;  
 Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSEDEEHTIITDTELPPLKLMHSFCADGPKADGPKAKMKRFFNITROCEEFYIGGCE 60  
 Db 1 DSEDEEHTIITDTELPPLKLMHSFCADGPKADGPKAKMKRFFNITROCEEFYIGGCE 60  
 QY 61 GNQRFESLECKKMCCTRDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120  
 Db 61 GNQRFESLECKKMCCTRDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120  
 QY 121 QCERFYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNANVNSLTPOSTKVPSSL 180  
 Db 121 QCERFYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNANVNSLTPOSTKVPSSL 180  
 QY 181 FEHGPSWCLTPADRGICRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECRLACK 240  
 Db 181 FEHGPSWCLTPADRGICRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECRLACK 240



XX FH Key Location/Qualifiers  
XX FT Domain 19..89  
XX FT /label = Kunitz domain  
XX FT /note= "Specifically claimed in Claim 18"  
XX FT Domain 90..160  
XX FT /label = Kunitz domain  
XX FT /note= "Specifically claimed in Claim 19 and Claim 21"  
XX PN US2003139339-A1.  
XX PD 24-JUL-2003.  
XX PF 15-OCT-2002; 2002US-00270478.  
XX PR 15-OCT-2001; 2001US-0328806P.  
XX PA (CREA/) CREASEY A.  
XX PI Creasey A;  
XX PD WPI; 2003-897354/82.  
XX DR Treating or preventing severe pneumonia by administering tissue factor  
XX PT pathway inhibitor (TFPI) or its analog to a patient having or is at risk  
XX PT of having severe pneumonia.  
XX PS Claim 20; SEQ ID NO 1; 14pp; English.  
XX PS The present invention relates to a method for treating or preventing  
XX CC severe pneumonia. The method comprises administering tissue factor  
XX CC pathway inhibitor (TFPI) or its analogue to a patient having, or at risk  
XX CC of having severe pneumonia. The method involves the use of continuous  
XX CC intravenous infusion of TFPI or TFPI analogue, preferably at low doses to  
XX CC avoid adverse side effects. The TFPI analogue is non-glycosylated N-L-  
XX CC alanyl-TFPI (ala-TFPI). It comprises a first or second Kunitz domain. The  
XX CC method is useful for treating or preventing severe pneumonia. The present  
XX CC sequence represents human TFPI protein.  
XX SQ Sequence 276 AA;  
Query Match 100.0%; Score 1528; DB 7; Length 276;  
Best Local Similarity 100.0%; Pred. No. 1.2e-129;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSEDEDEHTIITDTELPPLKLMHSFCAPKADGPKAIMKRRFFNFITRQCEEFYGGCE 60  
Db 1 DSEDEDEHTIITDTELPPLKLMHSFCAPKADGPKAIMKRRFFNFITRQCEEFYGGCE 60  
QY 61 GNONRFESLECKKMCCTRDNANRIIKTTLOEKPDPCFLEEDPGICRGYITRYFNNQTK 120  
Db 61 GNONRFESLECKKMCCTRDNANRIIKTTLOEKPDPCFLEEDPGICRGYITRYFNNQTK 120  
QY 121 QCFERFYGGCLGNMNNFETLECKNICEDGPGFQVDNYGTQLNAVNNSLTPQSTKVP 180  
Db 121 QCFERFYGGCLGNMNNFETLECKNICEDGPGFQVDNYGTQLNAVNNSLTPQSTKVP 180  
QY 181 FEHGPSWCLTPADRGLCRANENRFFYNSVIGKCRPFKYSGGCGNENFTSKQEC 240  
Db 181 FEHGPSWCLTPADRGLCRANENRFFYNSVIGKCRPFKYSGGCGNENFTSKQEC 240  
QY 241 KGFIQRISKGLIKTKRKRKQKVIAEIEIFVKNM 276  
Db 241 KGFIQRISKGLIKTKRKRKQKVIAEIEIFVKNM 276  
RESULT 5  
ADE80822  
ID ADE80822 standard; protein; 276 AA.  
XX ADE80822;  
AC ADE80822;  
XX ADE80822;  
DT 29-JAN-2004 (first entry)

XX Human tissue factor pathway inhibitor (TFPI) protein.  
XX DE Seeps; septic shock; tissue factor pathway inhibitor; TFPI;  
XX KW N-L-alanyl-TFPI; ala-TFPI; Kunitz domain; human; antibacterial;  
XX KW antiinflammatory.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT Domain 19..89  
XX FT /label = Kunitz domain  
XX FT /note= "Specifically claimed in Claim 3"  
XX FT Domain 90..160  
XX FT /label = Kunitz domain  
XX FT /note= "Specifically claimed in Claim 4 and Claim 6"  
XX PN US2003139340-A1.  
XX PD 24-JUL-2003.  
XX PF 04-FEB-2003; 2003US-00270479.  
XX PR 15-OCT-2001; 2001US-0328806P.  
XX PA (CREA/) CREASEY A.  
XX PI Creasey A;  
XX PD WPI; 2003-897355/82.  
XX DR Treating sepsis by administering TFPI or its analog by continuous  
XX PT intravenous infusion at dose rate equivalent to reference ala-TFPI at  
XX PT dose rate of less than 0.00025-0.050 mg/hr for at least 72 hours.  
XX PS Claim 5; SEQ ID NO 1; 27pp; English.  
XX PS The present invention relates to a method for treating or preventing  
XX CC sepsis or septic shock. The method comprises administering tissue factor  
XX CC pathway inhibitor (TFPI) or its analogue to a patient having, or at risk  
XX CC of having sepsis or septic shock. The method involves the use of  
XX CC continuous intravenous infusion of TFPI or TFPI analogue, preferably at  
XX CC low doses to avoid adverse side effects. The TFPI analogue is non-  
XX CC glycosylated N-L-alanyl-TFPI (ala-TFPI). It comprises a first or second  
XX CC Kunitz domain. The method is useful for treating or preventing sepsis or  
XX CC septic shock. The present sequence represents human TFPI protein.  
XX SQ Sequence 276 AA;  
Query Match 100.0%; Score 1528; DB 7; Length 276;  
Best Local Similarity 100.0%; Pred. No. 1.2e-129;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSEDEDEHTIITDTELPPLKLMHSFCAPKADGPKAIMKRRFFNFITRQCEEFYGGCE 60  
Db 1 DSEDEDEHTIITDTELPPLKLMHSFCAPKADGPKAIMKRRFFNFITRQCEEFYGGCE 60  
QY 61 GNONRFESLECKKMCCTRDNANRIIKTTLOEKPDPCFLEEDPGICRGYITRYFNNQTK 120  
Db 61 GNONRFESLECKKMCCTRDNANRIIKTTLOEKPDPCFLEEDPGICRGYITRYFNNQTK 120  
QY 121 QCFERFYGGCLGNMNNFETLECKNICEDGPGFQVDNYGTQLNAVNNSLTPQSTKVP 180  
Db 121 QCFERFYGGCLGNMNNFETLECKNICEDGPGFQVDNYGTQLNAVNNSLTPQSTKVP 180  
QY 181 FEHGPSWCLTPADRGLCRANENRFFYNSVIGKCRPFKYSGGCGNENFTSKQEC 240  
Db 181 FEHGPSWCLTPADRGLCRANENRFFYNSVIGKCRPFKYSGGCGNENFTSKQEC 240  
QY 241 KGFIQRISKGLIKTKRKRKQKVIAEIEIFVKNM 276  
Db 241 KGFIQRISKGLIKTKRKRKQKVIAEIEIFVKNM 276

## RESULT 6

AD120097  
ID AD120097 standard; protein; 276 AA.XX AC  
XX AC  
AD120097;

DT 22-APR-2004 (first entry)

XX DE Human TFPI.

XX tissue factor pathway inhibitor; TFPI; Antibacterial; Immunosuppressive;  
KW Antinflammatory; chronic inflammation; sepsis; shock;  
KW acute respiratory distress syndrome; ARDS.

XX OS Homo sapiens.

XX PN WO2003055442-A2.

XX PD 10-JUL-2003.

XX PF 15-OCT-2002; 2002WO-US032625.

XX PR 15-OCT-2001; 2001US-0328806P.

XX PA (CHIR ) CHIRON CORP.

XX PI Creasey AA;

XX PR WPI; 2003-902653/82.

XX PT Treating sepsis involves continuous intravenous infusion of tissue factor  
PT pathway inhibitor or tissue factor pathway inhibitor analog to a patient.

XX PS Claim 5; SEQ ID NO 1; 58pp; English.

XX CC The present invention relates to treating sepsis comprising continuous  
CC intravenous infusion of tissue factor pathway inhibitor (TFPI) or TFPI  
CC analog to a patient at a dose rate equivalent to administration of  
CC reference ala-TFPI. The method is useful for treating a patient suffering  
CC from sepsis, shock, or acute respiratory distress syndrome (ARDS), is  
CC useful for treating acute inflammation and for treating chronic or acute  
CC inflammation. The present sequence represents human TFPI.

XX SQ Sequence 276 AA;

Query Match 100.0%; Score 1528; DB 7; Length 276;  
Best Local Similarity 100.0%; Pred. No. 1.2e-129;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEHTIITDTELPPLKLMHSFCAPKADGPKAIIKMFNFFNTRQCEEFYGGCE 60

DB 1 DSEDEHTIITDTELPPLKLMHSFCAPKADGPKAIIKMFNFFNTRQCEEFYGGCE 60

QY 61 GQNRFSLECKKMCCTRDNANRIIKTTLOEKDPDFCFLEEDPGICRGYITRYFYNNQTK 120

DB 61 GQNRFSLECKKMCCTRDNANRIIKTTLOEKDPDFCFLEEDPGICRGYITRYFYNNQTK 120

QY 121 QCFERKYGCCLGNNMNFETLECKNICEDGPNGVQDNYGTQLNANNSLTPQSTKVPSSL 180

DB 121 QCFERKYGCCLGNNMNFETLECKNICEDGPNGVQDNYGTQLNANNSLTPQSTKVPSSL 180

QY 181 FEFGPSWCLTPADRGCLCRANENRPFYNSVIGKCRPFKYSYCGGNNFTSKQECRLACK 240

DB 181 FEFGPSWCLTPADRGCLCRANENRPFYNSVIGKCRPFKYSYCGGNNFTSKQECRLACK 240

QY 241 KGFIQRIKGGGLIKTKRKQRKQVIAEIEFVKNM 276

DB 241 KGFIQRIKGGGLIKTKRKQRKQVIAEIEFVKNM 276

## RESULT 7

ADQ76118

ADQ76118 standard; protein; 276 AA.

XX AC ADQ76118;

XX DT 21-OCT-2004 (first entry)

XX DE Human tissue factor pathway inhibitor protein.

XX KW Lyophilised; TFPI; tissue factor pathway inhibitor; glass forming agent;  
KW aggregation stability; antibacterial; immunosuppressive; sepsis; human.

XX OS Homo sapiens.

XX PN WO2004062646-A1.

XX PD 29-JUL-2004.

XX PF 08-JAN-2004; 2004WO-US000235.

XX PR 08-JAN-2003; 2003US-0438524P.

XX PR 13-AUG-2003; 2003US-0494547P.

XX PR 08-OCT-2003; 2003US-0509276P.

XX PR 20-OCT-2003; 2003US-0512092P.

XX PA (CHIR ) CHIRON CORP.

XX PI Chen B, Hora M;

XX PR WPI; 2004-561749/54.

XX PT Lyophilized composition with greater aggregation stability, useful in the

XX PS Claim 2; SEQ ID NO 1; 76pp; English.

XX CC The invention relates to a novel lyophilised composition of TFPI (tissue  
CC factor pathway inhibitor) or TFPI variant. The composition comprises TFPI  
CC or a TFPI variant and a carbohydrate or amino acid glass forming agent  
CC where the lyophilised composition has about 45% or greater aggregation  
CC stability. The invention further comprises: a TFPI composition, before  
CC lyophilisation, where the TFPI or TFPI variant is present in an aqueous  
CC formulation comprising a carbohydrate or amino acids glass forming agent,  
CC where the aqueous formulation has a pH of about 4 to about 8; and the  
CC lyophilised TFPI composition comprising a TFPI or TFPI variant and a  
CC citrate buffer, where the lyophilised composition has 45% or greater  
CC aggregation stability. The lyophilised TFPI composition has antibacterial  
CC and immunosuppressive activity. The lyophilised TFPI composition is  
CC useful in the treatment of sepsis. This sequence represents the human  
CC tissue factor pathway inhibitor protein of the invention.

XX SQ Sequence 276 AA;

Query Match 100.0%; Score 1528; DB 8; Length 276;  
Best Local Similarity 100.0%; Pred. No. 1.2e-129;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEHTIITDTELPPLKLMHSFCAPKADGPKAIIKMFNFFNTRQCEEFYGGCE 60

DB 1 DSEDEHTIITDTELPPLKLMHSFCAPKADGPKAIIKMFNFFNTRQCEEFYGGCE 60

QY 61 GQNRFSLECKKMCCTRDNANRIIKTTLOEKDPDFCFLEEDPGICRGYITRYFYNNQTK 120

DB 61 GQNRFSLECKKMCCTRDNANRIIKTTLOEKDPDFCFLEEDPGICRGYITRYFYNNQTK 120

QY 121 QCFERKYGCCLGNNMNFETLECKNICEDGPNGVQDNYGTQLNANNSLTPQSTKVPSSL 180

DB 121 QCFERKYGCCLGNNMNFETLECKNICEDGPNGVQDNYGTQLNANNSLTPQSTKVPSSL 180

QY 181 FEFGPSWCLTPADRGCLCRANENRPFYNSVIGKCRPFKYSYCGGNNFTSKQECRLACK 240

DB 181 FEFGPSWCLTPADRGCLCRANENRPFYNSVIGKCRPFKYSYCGGNNFTSKQECRLACK 240

QY	241	KGFIQRIKSGGLIKTKRKRKQVIAEIEIFVKNM	276
Db	241	KGFIQRIKSGGLIKTKRKRKQVIAEIEIFVKNM	276
RESULT 8			
ADQ76119			
ID	ADQ76119	standard; protein; 276 AA.	
XX	AC		
XX	ADQ76119;		
XX	DT	21-OCT-2004 (first entry)	
XX	XX		
DE	XX	Human tissue factor pathway inhibitor protein.	
XX	XX		
KW	XX	Aqueous composition; aggregation stability; oxidation;	
KW	XX	tissue factor pathway inhibitor; TPPI; solubilising agent; antioxidant;	
KW	XX	antibacterial; immunosuppressive; thrombolytic; vasotropic; cytostatic;	
KW	XX	sepsis; deep vein thrombosis; ischaemia; restenosis; cancer; unfolding;	
XX	XX	refolding; denaturation; human.	
OS	XX	Homo sapiens.	
XX	XX		
FN	XX	WO2004062689-A1.	
XX	XX		
PD	XX	29-JUL-2004.	
XX	XX		
PF	XX	08-JAN-2004; 2004WO-US000233.	
XX	XX		
PR	XX	08-JAN-2003; 2003US-0438519P.	
PR	XX	13-AUG-2003; 2003US-0494577P.	
PR	XX	08-OCT-2003; 2003US-0509260P.	
PR	XX	20-OCT-2003; 2003US-0512090P.	
XX	XX		
PA	XX	(CHIR ) CHIRON CORP.	
XX	XX		
PI	XX	Chen B;	
XX	XX		
DR	XX	WPI; 2004-561766/54.	
XX	XX		
PT	XX	Aqueous composition, useful to treat e.g. deep vein thrombosis, sepsis	
PT	XX	and cancer, comprises tissue factor pathway inhibitor or its variant, a	
PT	XX	solubilising agent (e.g. arginine) and an antioxidant (e.g. an oxygen	
PT	XX	displacement gas).	
XX	XX		
PS	XX	Claim 2; SEQ ID NO 1; 55pp; English.	
XX	XX		
CC	XX	The invention relates to a novel aqueous composition (having 45% or more	
CC	XX	aggregation stability, 45% or more oxidation stability and 4-8 pH). The	
CC	XX	composition comprises 0.05-15 mg/ml of a tissue factor pathway inhibitor	
CC	XX	(TPPI) or its variant, 50-600 mM of a solubilising agent (arginine or its	
CC	XX	analogue and/or lysine or its analogue) and an antioxidant (an oxygen	
CC	XX	displacement gas, an oxygen or free radical scavenger and/or a chelating	
CC	XX	agent). The invention further comprises a pharmaceutical composition	
CC	XX	comprising the aqueous composition. The aqueous composition has the	
CC	XX	following activities: antibacterial, immunosuppressive, thrombolytic,	
CC	XX	vasotropic, and cytostatic. The aqueous solution is useful to treat	
CC	XX	sepsis, deep vein thrombosis, ischaemia, restenosis and cancer. The use	
CC	XX	of a solubilising agent and an oxidant improves the stability of the	
CC	XX	aqueous compositions comprising TPPI or its variant. The aqueous	
CC	XX	compositions also resist other detrimental effects (e.g. unfolding,	
CC	XX	refolding and denaturation) that results in a loss of biological activity	
CC	XX	or in undesirable characteristics. This sequence represents a human	
XX	XX	tissue factor pathway inhibitor protein of the invention.	
XX	XX		
XX	XX	Sequence 276 AA;	
Query Match 100.0%; Score 1528; DB 8; Length 276;			
Best Local Similarity 100.0%; Pred. No. 1.2e-129;			
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	DSEDEHTIITDTELPPLKLMHSCAFKADGPKCKAIMKRRFFNIFTRQCEEFYGGCE	60

Db 2 DSEDEEHTIITDTLPLPLKLMHSFCAPKADDPCKAIMKRPFFNIFTRQCEEFYGGCE 61  
 Qy 61 GNQRFESLECKKMCCTRDANRIIKTTLQEKDPDFCFLEEDPGICRGYIITRYFYNNQTK 120  
 Db 62 GNQRFESLECKKMCCTRDANRIIKTTLQEKDPDFCFLEEDPGICRGYIITRYFYNNQTK 121  
 Qy 121 QCEPFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVPSSL 180  
 Db 122 QCEPFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVPSSL 181  
 Qy 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPPKYSGCGNENFTSKQECCLACK 240  
 Db 182 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPPKYSGCGNENFTSKQECCLACK 241  
 Qy 241 KGFIQIRISKGLIKTKRKRKQVVKIAYEEIFVKNM 276  
 Db 242 KGFIQIRISKGLIKTKRKRKQVVKIAYEEIFVKNM 277

## RESULT 10

AD80823  
 ID ADE80823 standard; protein; 277 AA.

AC ADE80823;

DT 29-JAN-2004 (first entry)

DE Human tissue factor pathway inhibitor (TFPI) analogue, ala-TFPI.

DE Sepsis; septic shock; tissue factor pathway inhibitor; TFPI;

KW N-L-alanyl-TFPI; ala-TFPI; TFPI analogue, Kunitz domain; human;

KW antibacterial; antiinflammatory.

OS Synthetic.

OS Homo sapiens.

XX US2003139340-A1.

XX 24-JUL-2003.

XX 04-FEB-2003; 2003US-00270479.

XX 15-OCT-2001; 2001US-0328806P.

XX (CREA/) CREASEY A.

XX Creasey A;

XX WPI; 2003-897355/82.

PT Treating sepsis by administering TFPI or its analog by continuous  
 PT intravenous infusion at dose rate equivalent to reference ala-TFPI at  
 PT dose rate of less than 0.0025-0.050 mg/kg/hr for at least 72 hours.

PS Disclosure; SEQ ID NO 2; 277p; English.

XX The present invention relates to a method for treating or preventing  
 CC sepsis or septic shock. The method comprises administering tissue factor  
 CC pathway inhibitor (TFPI) or its analogue to a patient having, or at risk  
 CC of having sepsis or septic shock. The method involves the use of  
 CC continuous intravenous infusion of TFPI or TFPI analogue, preferably at  
 CC low doses to avoid adverse side effects. The TFPI analogue is non-  
 CC glycosylated N-L-alanyl-TFPI (ala-TFPI). It comprises a first or second  
 CC Kunitz domain. The method is useful for treating or preventing sepsis or  
 CC septic shock. The present sequence represents human TFPI analogue, ala-  
 CC TFPI.

XX Sequence 277 AA;

Query Match 100.0%; Score 1528; DB 7; Length 277;

Best Local Similarity 100.0%; Pred. No. 1.2e-129;

Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTIITDTLPLPLKLMHSFCAPKADDPCKAIMKRPFFNIFTRQCEEFYGGCE 60  
 Db 2 DSEDEEHTIITDTLPLPLKLMHSFCAPKADDPCKAIMKRPFFNIFTRQCEEFYGGCE 61  
 Qy 61 GNQRFESLECKKMCCTRDANRIIKTTLQEKDPDFCFLEEDPGICRGYIITRYFYNNQTK 120  
 Db 62 GNQRFESLECKKMCCTRDANRIIKTTLQEKDPDFCFLEEDPGICRGYIITRYFYNNQTK 121  
 Qy 121 QCEPFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVPSSL 180  
 Db 122 QCEPFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVPSSL 181  
 Qy 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPPKYSGCGNENFTSKQECCLACK 240  
 Db 182 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPPKYSGCGNENFTSKQECCLACK 241  
 Qy 241 KGFIQIRISKGLIKTKRKRKQVVKIAYEEIFVKNM 276  
 Db 242 KGFIQIRISKGLIKTKRKRKQVVKIAYEEIFVKNM 277

## RESULT 11

AD120098

ID AD120098 standard; protein; 277 AA.

AC AD120098;

DT 22-APR-2004 (first entry)

DE Human Ala-TFPI analog.

KW tissue factor pathway inhibitor; TFPI; Antibacterial; Immunosuppressive;

KW Antiinflammatory; chronic inflammation; sepsis; shock;

KW acute respiratory distress syndrome; ARDS.

OS Homo sapiens.

XX WO2003055442-A2.

XX 10-JUL-2003.

XX 15-OCT-2002; 2002WO-US032625.

XX 15-OCT-2001; 2001US-0328806P.

XX (CHIR ) CHIRON CORP.

XX Creasey AA;

XX WPI; 2003-902653/82.

PT Treating sepsis involves continuous intravenous infusion of tissue factor  
 PT pathway inhibitor or tissue factor pathway inhibitor analog to a patient.

PS Disclosure; SEQ ID NO 2; 58pp; English.

XX The present invention relates to treating sepsis comprising continuous  
 CC intravenous infusion of tissue factor pathway inhibitor (TFPI) or TFPI  
 CC analog to a patient at a dose rate equivalent to administration of  
 CC reference ala-TFPI. The method is useful for treating a patient suffering  
 CC from sepsis, shock, or acute respiratory distress syndrome (ARDS), is  
 CC useful for treating acute inflammation and for treating chronic or acute  
 CC inflammation. The present sequence represents human Ala-TFPI analog.

XX Sequence 277 AA;

Query Match 100.0%; Score 1528; DB 7; Length 277;

Best Local Similarity 100.0%; Pred. No. 1.2e-129;

Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTIITDTLPLPLKLMHSFCAPKADDPCKAIMKRPFFNIFTRQCEEFYGGCE 60

Db 2 DSEDEEHTIITDTLPLPLKLMHSFCAPKADDPCKAIMKRPFFNIFTRQCEEFYGGCE 61

QY 61 GNQRFESLECKKQVCTRDNANRIIKTTLOQKPDPCFLEEDPGICRGYITRYFYNNQTK 120  
 DB 62 GNQRFESLECKKQVCTRDNANRIIKTTLOQKPDPCFLEEDPGICRGYITRYFYNNQTK 121  
 QY 121 QCFERFKYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNNAVNSLTPQSTKVPSL 180  
 DB 122 QCFERFKYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNNAVNSLTPQSTKVPSL 181  
 QY 181 FEFHGPSWCLTPADRGGLCRANENRFFYNSVIGKCRPFKYSGCGGNENFTSKQECIRACK 240  
 DB 182 FEFHGPSWCLTPADRGGLCRANENRFFYNSVIGKCRPFKYSGCGGNENFTSKQECIRACK 241  
 QY 241 KGFIQRISKGLIKTKRKRKQVIAVEEIEFVKNM 276  
 DB 242 KGFIQRISKGLIKTKRKRKQVIAVEEIEFVKNM 277

## RESULT 12

AAR67994  
 ID AAR67994 standard; protein; 304 AA.

AC AAR67994;

DT 25-MAR-2003 (revised)  
 DT 13-AUG-1995 (first entry)

XX Tissue factor pathway inhibitor.

XX Yeast aspartic protease 3; YAP3; signal peptide; protein secretion;  
 KW tissue factor pathway inhibitor; TPPI.

XX Homo sapiens.

FH Key Location/Qualifiers  
 FT Peptide 1..28  
 FT /label= Sig\_peptide  
 FT /note= "TPPI signal peptide"

XX WO9502059-A1.

XX 19-JAN-1995.

XX 08-JUL-1994; 94WO-DK000281.

XX 08-JUL-1993; 93DK-00000828.

XX (NOVO ) NOVO-NORDISK AS.

XX Christiansen L, Petersen JG;

XX WPI; 1995-066903/09.

XX N-PSDB; AAQ81396.

XX DNA construct encoding the yeast aspartic protease 3 signal peptide -  
 PT provides improved secretion of proteins in transformed yeast cells, such  
 PT as aprotinin and insulin.

PS Disclosure; Page 27-28; 56pp; English.

XX A SalI fragment encoding human tissue factor pathway inhibitor (TPPI) is  
 CC given in AAQ81396. It was used to construct expression vectors allowing  
 CC production of TPPI in Saccharomyces cerevisiae as fusions to the yeast  
 CC aspartic protease 3 (YAP3) signal peptide, facilitating secretion of the  
 CC recombinant TPPI. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 304 AA;

Query Match 100.0%; Score 1528; DB 2; Length 304;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-129;  
 Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTITDTLPLKLMHSFCAPKADGFCFKALMKRFFNIFTRQCEEFYGGCE 60

DB 29 DSEDEEHTITDTLPLKLMHSFCAPKADGFCFKALMKRFFNIFTRQCEEFYGGCE 88  
 QY 61 GNQRFESLECKKQVCTRDNANRIIKTTLOQKPDPCFLEEDPGICRGYITRYFYNNQTK 120  
 DB 89 GNQRFESLECKKQVCTRDNANRIIKTTLOQKPDPCFLEEDPGICRGYITRYFYNNQTK 148  
 QY 121 QCFERFKYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNNAVNSLTPQSTKVPSL 180  
 DB 149 QCFERFKYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNNAVNSLTPQSTKVPSL 208  
 QY 181 FEFHGPSWCLTPADRGGLCRANENRFFYNSVIGKCRPFKYSGCGGNENFTSKQECIRACK 240  
 DB 209 FEFHGPSWCLTPADRGGLCRANENRFFYNSVIGKCRPFKYSGCGGNENFTSKQECIRACK 268  
 QY 241 KGFIQRISKGLIKTKRKRKQVIAVEEIEFVKNM 276  
 DB 269 KGFIQRISKGLIKTKRKRKQVIAVEEIEFVKNM 304

## RESULT 13

AAR81884  
 ID AAR81884 standard; protein; 304 AA.

AC AAR81884;

DT 18-MAR-1996 (first entry)

XX Lipoprotein-associated coagulation inhibitor (LACI).

XX Lipoprotein-associated coagulation inhibitor; LACI; kallikrein;  
 KW inhibitor; KIP; Kunitz domain; hereditary angioedema.

XX Homo sapiens.

FH Key Location/Qualifiers  
 FT Peptide 1..28  
 FT /label= sig\_peptide  
 FT Domain 50..107  
 FT /note= "Kunitz domain LACI-K1"  
 FT Domain 121..178  
 FT /note= "Kunitz domain LACI-K2"  
 FT Domain 213..270  
 FT /note= "Kunitz domain LACI-K3"

XX WO9521601-A2.

XX 17-AUG-1995.

XX 11-JAN-1995; 95WO-US000299.

XX 11-JAN-1994; 94US-00179964.

XX 10-MAR-1994; 94US-00208264.

XX (PROT-) PROTEIN ENG CORP.

XX Markland W, Ladner RC;

XX WPI; 1995-292934/38.

XX Kallikrein inhibiting proteins comprising a Kunitz domain homologous to  
 CC bovine pancreatic trypsin inhibitor - useful for preventing or treating  
 CC disorders attributable to excessive kallikrein activity, eg. in  
 CC hereditary angioedema.

PS Disclosure; Page 24; 46pp; English.

XX AAR81884 is the human lipoprotein-associated coagulation inhibitor LACI.  
 CC The Kunitz domain, LACI-K1, of LACI is a kallikrein inhibiting protein  
 CC (KIP) upon which the claimed KIPs of the invention are based. The KIPs  
 CC can be used for treating or preventing disorders attributable to  
 CC excessive kallikrein activity, e.g. hereditary angioedema. The KIPs can  
 CC also be used for activating, purifying and in vivo imaging of kallikrein



```
XX SQ Sequence 304 AA;
Query Match 100.0%; Score 1528; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSEDEEHTIITDELPLPLKLMHSCAFKADGPKCAIMKRFFNIFTRQCEEFYGGCE 60
DB 29 DSEDEEHTIITDELPLPLKLMHSCAFKADGPKCAIMKRFFNIFTRQCEEFYGGCE 88
QY 61 GNQNFESLECKKMCCTRDNANRIIKTTLOQEKDPFCFLEEDPGICRGVITFYFNNQTK 120
DB 89 GNQNFESLECKKMCCTRDNANRIIKTTLOQEKDPFCFLEEDPGICRGVITFYFNNQTK 148
QY 121 QCEPFKYGGCLGNMNFETLECKNICEDGPNQFVDNYGTOLNANNVNSLTQSTKVP 180
DB 149 QCEPFKYGGCLGNMNFETLECKNICEDGPNQFVDNYGTOLNANNVNSLTQSTKVP 208
QY 181 FEHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKOECL 240
DB 209 FEHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKOECL 268
QY 241 KGFIQIRISKGGLIKTKRKRKQKVIAEIEFVKNM 276
DB 269 KGFIQIRISKGGLIKTKRKRKQKVIAEIEFVKNM 304

RESULT 14
AA49557
ID AA49557 standard; protein; 304 AA.
XX AC AA49557;
XX DT 13-JAN-2000 (first entry)
XX DE Human lipoprotein associated coagulation inhibitor protein sequence.
XX KW Human; coding sequence polymorphism; vascular pathology gene;
XX KW polymorphic site; phenotype correlation; forensic; paternity testing;
XX KW medicine; genetic analysis; vascular disease.
XX OS Homo sapiens.
XX PN WO9950454-A2.
XX PD 07-OCT-1999.
XX PF 26-MAR-1999; 99WO-US006473.
XX PR 01-APR-1998; 98US-00054272.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PI Lander ES, Daley GQ, Cargill M, Ireland JS, Rozen SG;
XX WPI; 1999-620066/53.
XX DR N-PSDB; AA232166.
XX PT Determination of polymorphisms in genes, especially those identifying
XX PT predisposition to vascular disease.
XX PS Disclosure; Fig 10; 134pp; English.
XX CC AA232159 to AA232194 represent reference alleles for specifically claimed
XX CC nucleic acid sequences from the present invention which comprise
XX CC polymorphic sites as given in a table in the specification, selected from
XX CC 92 single nucleotide polymorphisms in which the nucleotide at the
XX CC polymorphic site is different from a nucleotide at the same site in a
XX CC reference allele. The nucleic acids, and primers and probes, are used to
XX CC identify polymorphisms, which may predispose an individual to disease,
XX CC especially a vascular disease. They can also be used in phenotype
XX CC correlations, forensics, paternity testing, medicine or genetic analysis.
```

```
CC AA49550 to AA49573 represent the proteins which correspond to some of
CC the reference alleles
XX SQ Sequence 304 AA;
Query Match 100.0%; Score 1528; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSEDEEHTIITDELPLPLKLMHSCAFKADGPKCAIMKRFFNIFTRQCEEFYGGCE 60
DB 29 DSEDEEHTIITDELPLPLKLMHSCAFKADGPKCAIMKRFFNIFTRQCEEFYGGCE 88
QY 61 GNQNFESLECKKMCCTRDNANRIIKTTLOQEKDPFCFLEEDPGICRGVITFYFNNQTK 120
DB 89 GNQNFESLECKKMCCTRDNANRIIKTTLOQEKDPFCFLEEDPGICRGVITFYFNNQTK 148
QY 121 QCEPFKYGGCLGNMNFETLECKNICEDGPNQFVDNYGTOLNANNVNSLTQSTKVP 180
DB 149 QCEPFKYGGCLGNMNFETLECKNICEDGPNQFVDNYGTOLNANNVNSLTQSTKVP 208
QY 181 FEHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKOECL 240
DB 209 FEHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKOECL 268
QY 241 KGFIQIRISKGGLIKTKRKRKQKVIAEIEFVKNM 276
DB 269 KGFIQIRISKGGLIKTKRKRKQKVIAEIEFVKNM 304

RESULT 15
ADF09568
ID ADF09568 standard; protein; 304 AA.
XX AC ADF09568;
XX DT 12-FEB-2004 (first entry)
XX DE Human tissue factor pathway inhibitor SEQ ID NO:69.
XX KW human; protein-protein interaction; virucide; cytostatic; vaccine;
XX KW human papilloma virus; HPV; cancer.
XX OS Homo sapiens.
XX PN WO2003068940-A2.
XX PD 21-AUG-2003.
XX PF 14-FEB-2003; 2003WO-US004594.
XX PR 14-FEB-2002; 2002US-0356911P.
XX PA (CURA-) CURAGEN CORP.
XX PA (HOFF ) HOFFMANN LA ROCHE INC.
XX PI Jackson A, Ooi CE, Lewin DA, Cuthill S;
XX WPI; 2003-689668/65.
XX DR N-PSDB; ADF09675.
XX PT New purified complex comprising a first polypeptide and a second
XX PT polypeptide, useful for identifying agents for treating/preventing a
XX PT condition involving altered level of the complex e.g. human papilloma
XX PT virus infection, or cancer.
XX PS Example 3; SEQ ID NO 69; 156pp; English.
XX CC The invention relates to a novel purified complex comprising a first
XX CC polypeptide and a second polypeptide, where the polypeptides comprise
XX CC defined amino acid sequences listed in the specification, and where the
XX CC first polypeptide binds to the second polypeptide. A complex of the
XX CC invention has virucide and cytostatic activity, and may have a use as a
```

CC vaccine. The complex is useful for identifying agents for treating or  
CC preventing a conditions involving altered level of the complex, e.g.  
CC human papilloma virus (HPV) infection, or cancer. The compositions,  
CC antibodies, vectors and methods are useful for treating such diseases.  
CC The sequences shown in ADF09500-ADF09583 represent proteins of the  
CC invention.

XX

SQ Sequence 304 AA;

Query Match 100.0%; Score 1528; DB 7; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.4e-129;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	29	DSEEDDEHTIIITDTELPPLKLMHSCAFKADGPKCKAIWKRFNFNITRQCEEFYGGCE	88
QY	61	GNQNPESLECKKCTRDNANRIIKTTLQEKPDPCFLEEDPGICRGYITRYFYNNQTK	120
Db	89	GNQNPESLECKKCTRDNANRIIKTTLQEKPDPCFLEEDPGICRGYITRYFYNNQTK	148
QY	121	QCERFKYGGCLGNMNFLECKNICEDGPNQFQVDNYGTOLNANNSLTPQSTKVPSL	180
Db	149	QCERFKYGGCLGNMNFLECKNICEDGPNQFQVDNYGTOLNANNSLTPQSTKVPSL	208
QY	181	FEFHGPSWCLTPADRGCLCHANENRFYNSVIGKCRPFKYSGCGNENNFTSKQECCLACK	240
Db	209	FEFHGPSWCLTPADRGCLCHANENRFYNSVIGKCRPFKYSGCGNENNFTSKQECCLACK	268
QY	241	KGFIOIRISKGGLIKTKRKKKORVKIAYEEIFVKNM	276
Db	269	KGFIOIRISKGGLIKTKRKKKORVKIAYEEIFVKNM	304

Search completed: April 16, 2005, 03:26:51  
Job time : 176 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2005, 03:21:23 ; Search time 43 Seconds  
(without alignments)  
479.143 Million cell updates/sec

Title: US-10-753-079-1

Perfect score: 1528

Sequence: 1 DSEDEEHTITDTEPLK.....RKRKKQVKIAYEISIFVKQM 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pap.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pap.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pap.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pap.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1528	100.0	276	2	US-08-796-850-1
2	1528	100.0	276	4	US-09-766-778-1
3	1528	100.0	277	1	US-07-844-297-1
4	1528	100.0	304	1	US-08-026-145-2
5	1528	100.0	304	1	US-08-446-646-9
6	1528	100.0	304	1	US-08-676-125A-18
7	1528	100.0	304	2	US-09-136-012A-18
8	1528	100.0	304	3	US-08-676-124-1
9	1528	100.0	304	3	US-08-208-264A-25
10	1528	100.0	304	3	US-09-414-878-1
11	1528	100.0	304	3	US-09-240-136-1
12	1528	100.0	304	3	US-09-421-097-25
13	1528	100.0	304	4	US-09-638-770A-1
14	1528	100.0	304	4	US-09-054-272-16
15	1528	100.0	304	6	5466783-2
16	1528	100.0	304	6	5466783-2
17	1528	100.0	352	3	US-08-854-764-2
18	1528	100.0	352	5	PCT-US95-09377-2
19	1528	100.0	381	4	US-09-949-016-7400
20	1525	99.8	276	1	US-08-437-841-9
21	1525	99.8	276	1	US-08-286-521-9
22	1525	99.8	276	1	US-08-436-175-9
23	1525	99.8	276	3	US-08-854-764-3
24	1525	99.8	276	3	US-08-943-682-9
25	1525	99.8	276	4	US-09-741-106-9
26	1525	99.8	276	5	PCT-US95-09377-3
27	1525	99.8	276	5	PCT-US95-09464-9

28. 1522 99.6 304 3 US-09-054-782-2 Sequence 2, Appli  
29. 1522 99.6 304 4 US-09-627-676-2 Sequence 2, Appli  
30. 1522 99.6 304 4 US-10-377-817-2 Sequence 2, Appli  
31. 1521 99.3 276 1 US-07-828-920A-1 Sequence 1, Appli  
32. 1517 99.3 304 4 US-09-763-565-2 Sequence 2, Appli  
33. 1507 98.6 304 4 US-09-763-565-4 Sequence 4, Appli  
34. 1447.5 94.7 291 4 US-10-000-489-48 Sequence 48, Appli  
35. 1444.5 94.5 291 4 US-10-000-489-52 Sequence 52, Appli  
36. 1180.5 77.3 213 6 5466783-25 Patent No. 5466783  
37. 1180.5 77.3 213 6 5466783-25 Patent No. 5466783  
38. 900 58.9 189 1 US-07-828-920A-7 Sequence 7, Appli  
39. 897 58.7 161 1 US-08-437-841-19 Sequence 19, Appli  
40. 897 58.7 161 1 US-08-286-521-19 Sequence 19, Appli  
41. 897 58.7 161 1 US-08-436-175-19 Sequence 19, Appli  
42. 897 58.7 161 3 US-08-943-682-19 Sequence 19, Appli  
43. 897 58.7 161 4 US-09-741-106-19 Sequence 19, Appli  
44. 897 58.7 161 5 PCT-US95-09464-19 Sequence 19, Appli  
45. 834 54.6 183 1 US-07-828-920A-5 Sequence 5, Appli

#### ALIGNMENTS

#### RESULT 1

US-08-796-850-1  
; Sequence 1, Application US/08796850  
; Patent No. 5981471  
; GENERAL INFORMATION:  
; APPLICANT: Papathanassiou, Adonia E  
; APPLICANT: Green, Shawn J.  
; TITLE OF INVENTION: Compositions and Methods for Inhibiting  
; TITLE OF INVENTION: Cellular Proliferation  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: U.S.A.  
; ZIP: 30303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/796,850  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Greene, Jamie L.  
; REGISTRATION NUMBER: 32,467  
; REFERENCE/DOCKET NUMBER: 05213-0290  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 818-3700  
; TELEFAX: (404) 818-3799  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 276 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: Active-site  
; LOCATION: 2..3  
; OTHER INFORMATION: /note= "Site of partial  
; phosphorylation"



Db 61 GQNRPFESLECKKMTDNRNRIKTTLQOEKDPFCLEEDPGICRGYITRYFNNQTK 120  
QY 121 QCRFKYGGCLGNMNNFETLECKNICEDGPNFGVDNYGTQLNAVNSLTQSTKVPSSL 180  
Db 121 QCRFKYGGCLGNMNNFETLECKNICEDGPNFGVDNYGTQLNAVNSLTQSTKVPSSL 180  
QY 181 FEFHPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNNFTSKOECLACK 240  
Db 181 FEFHPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNNFTSKOECLACK 240  
QY 241 KGFIORISKGLIKTKRRKKQKVIAEIEFVKNM 276  
Db 241 KGFIORISKGLIKTKRRKKQKVIAEIEFVKNM 276

## RESULT 3

US-07-844-297-1  
; Sequence 1, Application US/07844297  
; Patent No. 5212091  
; GENERAL INFORMATION:  
; APPLICANT: Diaz-Collier, Judy A.  
; APPLICANT: Gustafson, Mark E.  
; APPLICANT: Wun, Tze-Chen  
; TITLE OF INVENTION: Method of Producing Tissue Factor  
; TITLE OF INVENTION: Pathway Inhibitor  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG  
; STREET: 800 N. Lindbergh Blvd.  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 63167

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/844,297  
; FILING DATE: 19920302  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyer, Scott J.  
; REGISTRATION NUMBER: 25,275  
; REFERENCE/DOCKET NUMBER: 07-21(819)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)694-3117  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 277 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-844-297-1

Query Match 100.0%; Score 1528; DB 1; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1.1e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTELPLKLMHSPCAKADGPKAIMKRPFFNIFTRQCEFIYGGCE 60  
Db 2 DSEDEEHTIITDTELPLKLMHSPCAKADGPKAIMKRPFFNIFTRQCEFIYGGCE 61  
QY 61 GQNRPFESLECKKMTDNRNRIKTTLQOEKDPFCLEEDPGICRGYITRYFNNQTK 120  
Db 62 GQNRPFESLECKKMTDNRNRIKTTLQOEKDPFCLEEDPGICRGYITRYFNNQTK 121  
QY 121 QCRFKYGGCLGNMNNFETLECKNICEDGPNFGVDNYGTQLNAVNSLTQSTKVPSSL 180  
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QY 181 FEFHPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNNFTSKOECLACK 240  
Db 182 FEFHPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNNFTSKOECLACK 241  
QY 241 KGFIORISKGLIKTKRRKKQKVIAEIEFVKNM 276  
Db 242 KGFIORISKGLIKTKRRKKQKVIAEIEFVKNM 277

## RESULT 4

US-08-026-145-2  
; Sequence 2, Application US/08026145  
; Patent No. 5378614  
; GENERAL INFORMATION:  
; APPLICANT: Petersen, Jens G. Liteke  
; APPLICANT: No. 5378614dfang, Ole Juul  
; TITLE OF INVENTION: Method for Making TFPI Analogues  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5378614o No. 5378614disk of No. 5378614th America, Inc.  
; STREET: 405 Lexington Avenue, Suite 6200  
; CITY: New York  
; STATE: N. Y.  
; COUNTRY: United States of America  
; ZIP: 10174-6201

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/026,145  
; FILING DATE: 19930302  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/828,920  
; FILING DATE: 27-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/DK/90/00212  
; FILING DATE: 17-AUG-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 4080/89  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Agtis, Cheryl H.  
; REGISTRATION NUMBER: 34086  
; REFERENCE/DOCKET NUMBER: 3321.214-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 867 0123  
; TELEFAX: 212 867 0298  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-026-145-2

Query Match 100.0%; Score 1528; DB 1; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 29 DSEDEEHTIITDTELPLKLMHSPCAKADGPKAIMKRPFFNIFTRQCEFIYGGCE 88  
QY 61 GQNRPFESLECKKMTDNRNRIKTTLQOEKDPFCLEEDPGICRGYITRYFNNQTK 120  
Db 89 GQNRPFESLECKKMTDNRNRIKTTLQOEKDPFCLEEDPGICRGYITRYFNNQTK 148  
QY 121 QCRFKYGGCLGNMNNFETLECKNICEDGPNFGVDNYGTQLNAVNSLTQSTKVPSSL 180  
Db 149 QCRFKYGGCLGNMNNFETLECKNICEDGPNFGVDNYGTQLNAVNSLTQSTKVPSSL 208

QY 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECCLACK 240  
DB 209 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECCLACK 268  
QY 241 KGFIORISKGGLIKTKRKRKQKVIAVEEIFVKNM 276  
DB 269 KGFIORISKGGLIKTKRKRKQKVIAVEEIFVKNM 304

## RESULT 5

US-08-446-646-9  
; Sequence 9, Application US/08446646  
; Patent No. 5726038  
; GENERAL INFORMATION:  
; APPLICANT: Christiansen, Lars  
; APPLICANT: Petersen, Jens G.  
; TITLE OF INVENTION: A DNA Construct Encoding the YAP3 Signal  
; TITLE OF INVENTION: Peptide  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 57260380 No. 5726038disk of No. 5726038th America, Inc.  
; STREET: 405 Lexington Avenue, 64th Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10174-6401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,646  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lambiris, Elias J.  
; REGISTRATION NUMBER: 33,728  
; REFERENCE/DOCKET NUMBER: 3987.204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-878-9655  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-446-646-9

Query Match 100.0%; Score 1528; DB 1; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKAIMKRFNFIFTRQCEEFYGGCE 60  
DB 29 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKAIMKRFNFIFTRQCEEFYGGCE 88  
QY 61 GQNRFESLECKKMCWTRDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120  
DB 89 GQNRFESLECKKMCWTRDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 148  
QY 121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSL 180  
DB 149 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSL 208  
QY 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECCLACK 240  
DB 209 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECCLACK 268  
QY 241 KGFIORISKGGLIKTKRKRKQKVIAVEEIFVKNM 276

DB 269 KGFIORISKGGLIKTKRKRKQKVIAVEEIFVKNM 304

## RESULT 6

US-08-676-125A-18  
; Sequence 18, Application US/08676125A  
; Patent No. 5795865  
; GENERAL INFORMATION:  
; APPLICANT: MARKLAND, William  
; APPLICANT: LADNER, Robert Charles  
; TITLE OF INVENTION: KALLIKREIN-INHIBITING "KUNITZ DOMAIN" PROTEINS AND ANALOGUES  
; NUMBER OF SEQUENCES: 70  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yankwich & Associates  
; STREET: 130 Bishop Allen Drive, fifth floor  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: United States of America  
; ZIP: 02139  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word for Windows 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/676,125A  
; FILING DATE: 25 September 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/00299  
; FILING DATE: 11 January 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/179,964  
; FILING DATE: 11 January 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/208,264  
; FILING DATE: 10 March 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YANKWICH, Leon R.  
; REGISTRATION NUMBER: 30,237  
; REFERENCE/DOCKET NUMBER: DYX-006.2P US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 491-4343  
; TELEFAX: (617) 491-8801  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-676-125A-18

Query Match 100.0%; Score 1528; DB 1; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKAIMKRFNFIFTRQCEEFYGGCE 60  
DB 29 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKAIMKRFNFIFTRQCEEFYGGCE 88  
QY 61 GQNRFESLECKKMCWTRDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 120  
DB 89 GQNRFESLECKKMCWTRDNANRIKTTLOQEKPDFCFLEEDPGICRGYITRYFYNNQTK 148  
QY 121 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSL 180  
DB 149 QCERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSL 208  
QY 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECCLACK 240  
DB 209 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKQECCLACK 268

QY 241 KGFIQIRISKGLIKTKRKRKQVIAEIEFVKNM 276  
DB 269 KGFIQIRISKGLIKTKRKRKQVIAEIEFVKNM 304

## RESULT 7

US-09-136-012A-18  
; Sequence 18, Application US/09136012A  
; Patent No. 5994125  
; GENERAL INFORMATION:  
; APPLICANT: DYAX CORP  
; APPLICANT: MARKLAND, William  
; APPLICANT: LADNER, Robert Charles  
; TITLE OF INVENTION: KALLIKREIN-INHIBITING "KUNITZ DOMAIN" PROTEINS  
; TITLE OF INVENTION: AND ANALOGUES THEREOF  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yankwich & Associates  
; STREET: 130 Bishop Allen Drive, fifth floor  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: United States of America  
; ZIP: 02139  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5-inch diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Microsoft Windows 98  
; SOFTWARE: Microsoft Word 97 SR-1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09136,012A  
; FILING DATE: 17-August-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/676,125  
; FILING DATE: 25-September-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/00299  
; FILING DATE: 11-January-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/208,264  
; FILING DATE: 10-March-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/179,964  
; FILING DATE: 11-January-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YANKWICH, Leon R.  
; REGISTRATION NUMBER: 30,237  
; NAME: ZWICKER, Kenneth P.  
; REGISTRATION NUMBER: 43,310  
; REFERENCE/DOCKET NUMBER: DYX-006.2P US-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 491-4343  
; TELEFAX: (617) 491-8801  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-136-012A-18

Query Match 100.0%; Score 1528; DB 2; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDELPLPKLMHSCAFKADGPKCAIMKRRFFNIFTRQCEEFYGGCE 60  
DB 29 DSEDEEHTIITDELPLPKLMHSCAFKADGPKCAIMKRRFFNIFTRQCEEFYGGCE 88  
QY 61 GQNRPFESLECKKMCCTRDNANRIKTTIQEKPDPFCFLEEDPGICRGVITRYFYNNQTK 120  
DB 89 GQNRPFESLECKKMCCTRDNANRIKTTIQEKPDPFCFLEEDPGICRGVITRYFYNNQTK 148

QY 121 QCERFKYGGCLGNMNFETLEECKNICEDGPNGFQVDNYGTOLNANNSLTPOSTKVPSSL 180  
DB 149 QCERFKYGGCLGNMNFETLEECKNICEDGPNGFQVDNYGTOLNANNSLTPOSTKVPSSL 208  
QY 181 FEFHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSCGGNENFTSKQECLRACK 240  
DB 209 FEFHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSCGGNENFTSKQECLRACK 268  
QY 241 KGFIQIRISKGLIKTKRKRKQVIAEIEFVKNM 276  
DB 269 KGFIQIRISKGLIKTKRKRKQVIAEIEFVKNM 304

## RESULT 8

US-08-676-124-1  
; Sequence 1, Application US/08676124  
; Patent No. 6010880  
; GENERAL INFORMATION:  
; APPLICANT: MARKLAND, William  
; APPLICANT: LADNER, Robert Charles  
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED  
; TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: United States of America  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/676,124  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/00298  
; FILING DATE: 11-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/179,658  
; FILING DATE: 11-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/208,265  
; FILING DATE: 10-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, IVER P.  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: MARKLAND-3B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-676-124-1

Query Match 100.0%; Score 1528; DB 3; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDELPLPKLMHSCAFKADGPKCAIMKRRFFNIFTRQCEEFYGGCE 60  
DB 29 DSEDEEHTIITDELPLPKLMHSCAFKADGPKCAIMKRRFFNIFTRQCEEFYGGCE 88  
QY 61 GQNRPFESLECKKMCCTRDNANRIKTTIQEKPDPFCFLEEDPGICRGVITRYFYNNQTK 120

Db 89 QNORFESLECKKMCCTRDNANRIKTTLOQEKDPDFCFLEEDPGICRGYITRYFYNNOTK 148  
Qy 121 QCEPFYKGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTOLNANNVNSLTPOSTKVPSSL 180  
Db 149 QCEPFYKGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTOLNANNVNSLTPOSTKVPSSL 208  
Qy 181 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 240  
Db 209 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 268  
Qy 241 KGFQIRISKGLIKTKRKRKKORVKIAYEEIFVKNM 276  
Db 269 KGFQIRISKGLIKTKRKRKKORVKIAYEEIFVKNM 304

## RESULT 9

US-08-208-264A-25  
; Sequence 25, Application US/08208264A  
; Patent No. 6057287  
; GENERAL INFORMATION:  
; APPLICANT: MARKLAND, William  
; APPLICANT: LADNER, Robert C.  
; TITLE OF INVENTION: KALIKREIN-BINDING "KUNITZ DOMAIN"  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yankwich & Associates  
; STREET: 130 Bishop Allen Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02139  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5-inch diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Microsoft Windows 95  
; SOFTWARE: Microsoft Word 97  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/208,264A  
; FILING DATE: 10-MAR-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/179,964  
; FILING DATE: 11-JAN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Leon R. Yankwich  
; REGISTRATION NUMBER: 30,237  
; REFERENCE/DOCKET NUMBER: DYX-006.1 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-491-4343  
; TELEFAX: 617-491-8801  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-208-264A-25

Query Match 100.0%; Score 1528; DB 3; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DSEDEEHTITDTELPPLKLMHSCAPKADGPGCKAIKMKFFNIFTRQCEEFYGGCE 60  
Db 29 DSEDEEHTITDTELPPLKLMHSCAPKADGPGCKAIKMKFFNIFTRQCEEFYGGCE 88  
Qy 61 QNORFESLECKKMCCTRDNANRIKTTLOQEKDPDFCFLEEDPGICRGYITRYFYNNOTK 120  
Db 89 QNORFESLECKKMCCTRDNANRIKTTLOQEKDPDFCFLEEDPGICRGYITRYFYNNOTK 148

Qy 121 QCEPFYKGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTOLNANNVNSLTPOSTKVPSSL 180  
Db 149 QCEPFYKGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTOLNANNVNSLTPOSTKVPSSL 208  
Qy 181 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 240  
Db 209 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKQECCLACK 268  
Qy 241 KGFQIRISKGLIKTKRKRKKORVKIAYEEIFVKNM 276  
Db 269 KGFQIRISKGLIKTKRKRKKORVKIAYEEIFVKNM 304  
RESULT 10  
US-09-414-878-1  
; Sequence 1, Application US/09414878  
; Patent No. 6071723  
; GENERAL INFORMATION:  
; APPLICANT: DYAX CORP  
; APPLICANT: MARKLAND, William  
; APPLICANT: LADNER, Robert C.  
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived  
; TITLE OF INVENTION: From The Kunitz Domains  
; NUMBER OF SEQUENCES: 139  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yankwich & Associates  
; STREET: 130 Bishop Allen Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02139  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5-inch diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Microsoft Windows 98  
; SOFTWARE: Microsoft Word 97 SR-1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/414,878  
; FILING DATE: (concurrently herewith)  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/240,136  
; FILING DATE: 29-JAN-1999  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/676,124  
; FILING DATE: 07-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/00298  
; FILING DATE: 11-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/208,265  
; FILING DATE: 10-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/179,685  
; FILING DATE: 11-JAN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YANKWICH, Leon R  
; REGISTRATION NUMBER: 30,237  
; NAME: ZWICKER, Kenneth P  
; REGISTRATION NUMBER: 43,310  
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-491-4343  
; TELEFAX: 617-491-8801  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-414-878-1



Query Match 100.0%; Score 1528; DB 3; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145; Indels 0; Gaps 0;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKCAIMKRPFFNIFTRQCEEFYGGCE 60  
DB 29 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKCAIMKRPFFNIFTRQCEEFYGGCE 88  
QY 61 GQNRFSLEBCKKMCCTRDANRIIKTTLOQEKDPFCFLEEDPGICRGVITRYFYNNQTK 120  
DB 89 GQNRFSLEBCKKMCCTRDANRIIKTTLOQEKDPFCFLEEDPGICRGVITRYFYNNQTK 148  
QY 121 QCERFKYGGCLGNMNNFETLECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSL 180  
DB 149 QCERFKYGGCLGNMNNFETLECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSL 208  
QY 181 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNNFTSKQECIRACK 240  
DB 209 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNNFTSKQECIRACK 268  
QY 241 KGFIQRIKSGGLIKTKRKRKQKVIAVEEIFVKNM 276  
DB 269 KGFIQRIKSGGLIKTKRKRKQKVIAVEEIFVKNM 304

## RESULT 11

US-09-240-136-1  
; Sequence 1, Application US/09240136  
; Patent No. 6103499  
; GENERAL INFORMATION:  
; APPLICANT: DVAX CORP  
; APPLICANT: MARKLAND, William  
; APPLICANT: LADNER, Robert C  
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived  
; TITLE OF INVENTION: From The Kunitz Domains  
; NUMBER OF SEQUENCES: 139  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yankwich & Associates  
; STREET: 130 Bishop Allen Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02139  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5-inch diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Microsoft Windows 98  
; SOFTWARE: Microsoft Word 97 SR-1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/240,136  
; FILING DATE: (concurrently herewith)  
; CLASSIFICATION:  
; APPLICATION NUMBER: 08/676,124  
; FILING DATE: 07-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/00298  
; FILING DATE: 11-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/208,265  
; FILING DATE: 10-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/179,685  
; FILING DATE: 11-JAN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YANKWICH, Leon R  
; REGISTRATION NUMBER: 30,237  
; NAME: ZWICKER, Kenneth P  
; REGISTRATION NUMBER: 43,310  
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-491-4343  
; TELEFAX: 617-491-8801

; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-240-136-1

Query Match 100.0%; Score 1528; DB 3; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKCAIMKRPFFNIFTRQCEEFYGGCE 60  
DB 29 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKCAIMKRPFFNIFTRQCEEFYGGCE 88  
QY 61 GQNRFSLEBCKKMCCTRDANRIIKTTLOQEKDPFCFLEEDPGICRGVITRYFYNNQTK 120  
DB 89 GQNRFSLEBCKKMCCTRDANRIIKTTLOQEKDPFCFLEEDPGICRGVITRYFYNNQTK 148  
QY 121 QCERFKYGGCLGNMNNFETLECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSL 180  
DB 149 QCERFKYGGCLGNMNNFETLECKNICEDGPNGFQVDNYGTQLNAVNNSLTPQSTKVPSL 208  
QY 181 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNNFTSKQECIRACK 240  
DB 209 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNNFTSKQECIRACK 268  
QY 241 KGFIQRIKSGGLIKTKRKRKQKVIAVEEIFVKNM 276  
DB 269 KGFIQRIKSGGLIKTKRKRKQKVIAVEEIFVKNM 304

## RESULT 12

US-09-421-097-25  
; Sequence 25, Application US/09421097  
; Patent No. 633402  
; GENERAL INFORMATION:  
; APPLICANT: MARKLAND, William  
; APPLICANT: LADNER, Robert C  
; TITLE OF INVENTION: KALLIKREIN-BINDING "KUNITZ DOMAIN"  
; TITLE OF INVENTION: PROTEINS AND ANALOGUES THEREOF  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yankwich & Associates  
; STREET: 130 Bishop Allen Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02139  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5-inch diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Microsoft Windows 98  
; SOFTWARE: Microsoft Word 97  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/421,097  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/208,264  
; FILING DATE: 10-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/179,964  
; FILING DATE: 11-JAN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Leon R. Yankwich  
; REGISTRATION NUMBER: 30,237  
; REFERENCE/DOCKET NUMBER: DYX-006.1 US-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-491-4343  
; TELEFAX: 617-491-8801

INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 304 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-421-097-25

Query Match 100.0%; Score 1528; DB 3; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSEDEHTIITDTELPPLKLMHSFCFAKADGPKCAIMKRFNFNFTQCEEFYGGCE 60  
DB 29 DSEDEHTIITDTELPPLKLMHSFCFAKADGPKCAIMKRFNFNFTQCEEFYGGCE 88  
QY 61 GQNRFSLECKKMTNRDANRIIKTTLOQKPDPCFLEEDPGICRGYITRYFNNQTK 120  
DB 89 GQNRFSLECKKMTNRDANRIIKTTLOQKPDPCFLEEDPGICRGYITRYFNNQTK 148  
QY 121 QCFERFYGGCLGNMNFETLEECNICEGDPNGFQVDNYGTOLNANNSLTPQSTKVP 180  
DB 149 QCFERFYGGCLGNMNFETLEECNICEGDPNGFQVDNYGTOLNANNSLTPQSTKVP 208  
QY 181 FEFHGPSWCLTPADRGGLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSQECL 240  
DB 209 FEFHGPSWCLTPADRGGLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSQECL 268  
QY 241 KGFIORISKGGLIKTKRKKQKVIAEIEIFVKNM 276  
DB 269 KGFIORISKGGLIKTKRKKQKVIAEIEIFVKNM 304

## RESULT 13

US-09-638-770A-1  
Sequence 1, Application US/09638770A  
Patent No. 6423499

## GENERAL INFORMATION:

APPLICANT: DYAX CORP  
MARKLAND, William  
LADNER, Robert C  
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived  
FROM THE KUNITZ DOMAINS  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Yankwich & Associates  
STREET: 130 Bishop Allen Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02139

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5-inch diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Microsoft Windows 98  
SOFTWARE: Microsoft Word 97 SR-1  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/638,770A  
FILING DATE: 15-Aug-2000  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/676,124  
FILING DATE: 07-JAN-1997  
APPLICATION NUMBER: PCT/US95/00298  
FILING DATE: 11-JAN-1995  
APPLICATION NUMBER: 08/208,265  
FILING DATE: 10-MAR-1994  
APPLICATION NUMBER: 08/179,685  
FILING DATE: 11-JAN-1994

## ATTORNEY/AGENT INFORMATION:

NAME: ZWICKER, Kenneth P  
REGISTRATION NUMBER: 43,310

REFERENCE/DOCKET NUMBER: DYX-007.2P US-1

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-491-4343  
TELEFAX: 617-491-8801

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 304 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-638-770A-1

Query Match 100.0%; Score 1528; DB 4; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSEDEHTIITDTELPPLKLMHSFCFAKADGPKCAIMKRFNFNFTQCEEFYGGCE 60  
DB 29 DSEDEHTIITDTELPPLKLMHSFCFAKADGPKCAIMKRFNFNFTQCEEFYGGCE 88  
QY 61 GQNRFSLECKKMTNRDANRIIKTTLOQKPDPCFLEEDPGICRGYITRYFNNQTK 120  
DB 89 GQNRFSLECKKMTNRDANRIIKTTLOQKPDPCFLEEDPGICRGYITRYFNNQTK 148  
QY 121 QCFERFYGGCLGNMNFETLEECNICEGDPNGFQVDNYGTOLNANNSLTPQSTKVP 180  
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QY 181 FEFHGPSWCLTPADRGGLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSQECL 240  
DB 209 FEFHGPSWCLTPADRGGLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSQECL 268  
QY 241 KGFIORISKGGLIKTKRKKQKVIAEIEIFVKNM 276  
DB 269 KGFIORISKGGLIKTKRKKQKVIAEIEIFVKNM 304

## RESULT 14

US-09-054-272-16  
Sequence 16, Application US/09054272  
Patent No. 6692909

## GENERAL INFORMATION:

APPLICANT: Lander, Eric S.  
APPLICANT: Daley, George O.  
APPLICANT: Cargill, Michele  
APPLICANT: Ireland, James S.  
APPLICANT: Rozen, Steven G.  
TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS  
IN VASCULAR PATHOLOGY GENES  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/054,272  
FILING DATE: 01-APR-1998  
CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia

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; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI98-05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-09-054-272-16

Query Match 100.0%; Score 1528; DB 4; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTLPLPLKLMHSFCAPKADGPKAIMKRFFNIFTRQCEEFYGGCE 60
DB 29 DSEDEEHTIITDTLPLPLKLMHSFCAPKADGPKAIMKRFFNIFTRQCEEFYGGCE 88
QY 61 GQNRFSLEECKKWCTRDNANRIIKTTLQQEKDPDFCFLEEDPGICRGYITRYFYNNQTK 120
DB 89 GQNRFSLEECKKWCTRDNANRIIKTTLQQEKDPDFCFLEEDPGICRGYITRYFYNNQTK 148
QY 121 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVPSL 180
DB 149 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVPSL 208
QY 181 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNENNFTSKQECCLRACK 240
DB 209 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNENNFTSKQECCLRACK 268
QY 241 KGFIQIRISKGGGLIKTKRKRKKQKVIAEIEIFVKNM 276
DB 269 KGFIQIRISKGGGLIKTKRKRKKQKVIAEIEIFVKNM 304

Search completed: April 16, 2005, 03:29:35
Job time : 44 secs
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Query Match 100.0%; Score 1528; DB 6; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GQNRFSLEECKKWCTRDNANRIIKTTLQQEKDPDFCFLEEDPGICRGYITRYFYNNQTK 120
DB 89 GQNRFSLEECKKWCTRDNANRIIKTTLQQEKDPDFCFLEEDPGICRGYITRYFYNNQTK 148
QY 121 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVPSL 180
DB 149 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTQLNAVNNSLTPQSTKVPSL 208
QY 181 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNENNFTSKQECCLRACK 240
DB 209 FEFHGPSWCLTPADRGCLCRANENRFFYNSVIGKCRPFKYSGCGGNENNFTSKQECCLRACK 268
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DB 269 KGFIQIRISKGGGLIKTKRKRKKQKVIAEIEIFVKNM 304
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RESULT 15
5466783-2
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chien, Kretzmer, Kuniko K.; Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO: 2:
; LENGTH: 304
5466783-2
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Query Match 100.0%; Score 1528; DB 6; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTLPLPLKLMHSFCAPKADGPKAIMKRFFNIFTRQCEEFYGGCE 60
DB 29 DSEDEEHTIITDTLPLPLKLMHSFCAPKADGPKAIMKRFFNIFTRQCEEFYGGCE 88
QY 61 GQNRFSLEECKKWCTRDNANRIIKTTLQQEKDPDFCFLEEDPGICRGYITRYFYNNQTK 120
DB 89 GQNRFSLEECKKWCTRDNANRIIKTTLQQEKDPDFCFLEEDPGICRGYITRYFYNNQTK 148
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 16, 2005, 03:16:28 ; Search time 60 Seconds  
(without alignments)  
2355.564 Million cell updates/sec

Title: US-10-753-079-1

Perfect score: 1528

Sequence: 1 DSEDEBHTITDTPLPLK.....RKRKQKVKIAYEIVFVKNM 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1528	100.0	304	1 TPPI_HUMAN	P10646 homo sapien
2	1447	94.7	304	1 TPPI_MACMU	Q28864 macaca mula
3	1127	73.8	300	1 TPPI_RABIT	P19761 oryctolagus
4	993	65.0	396	2 Q28874	Q28874 canis famil
5	934.5	61.2	302	1 TPPI_RAT	Q02445 rattus norv
6	886	58.0	306	1 TPPI_MOUSE	O54819 mus musculu
7	607	39.7	235	2 Q8BSB7	Q8BSB7 mus musculu
8	607	39.7	235	2 Q8CI80	Q8CI80 mus musculu
9	537.5	35.2	279	2 Q7Z342	Q7Z342 brachydanio
10	518	33.9	287	2 Q93424	Q93424 cyprinus ca
11	463	30.3	224	2 Q7T025	Q7T025 xenopus lae
12	446	29.2	277	2 Q8AYE1	Q8AYE1 brachydanio
13	414.5	27.1	759	2 Q8IT91	Q8IT91 ancylostoma
14	392	25.7	234	2 Q7YRQ8	Q7YRQ8 bos taurus
15	388.5	25.4	2419	2 Q7PFX21	Q7PFX21 anopheles g
16	384.5	25.2	235	1 TPPI_HUMAN	P48307 homo sapien
17	378.5	24.8	224	2 Q8NAK6	Q8NAK6 homo sapien
18	373	24.4	3198	2 Q8U8G8	Q8U8G8 manduca sex
19	360	23.6	2772	2 Q8VAV4	Q8VAV4 drosophila
20	360	23.6	2776	2 Q869A0	Q869A0 drosophila
21	360	23.6	2894	2 Q7KRX2	Q7KRX2 drosophila
22	360	23.6	2898	2 Q86829	Q86829 drosophila
23	358.5	23.5	1487	2 Q8MPV5	Q8MPV5 caenorhabdi
24	355.5	23.3	1558	2 Q8I710	Q8I710 caenorhabdi
25	355.5	23.3	2167	2 Q76840	Q76840 caenorhabdi
26	353	23.1	230	1 TPPI_MOUSE	O35536 mus musculu
27	351.5	23.0	2174	2 Q8GQR0	Q8GQR0 drosophila
28	350.5	22.9	2225	2 Q45881	Q45881 caenorhabdi
29	347	22.7	1474	2 Q62504	Q62504 caenorhabdi
30	341.5	22.3	327	2 Q6IND9	Q6IND9 xenopus lae
31	341	22.3	230	2 Q8CF99	Q8CF99 rattus norv

#### ALIGNMENTS

##### RESULT 1

ID	TFPI_HUMAN	STANDARD;	PRT;	304 AA.
AC	P10646; O95103;			
DT	01-JUL-1989 (Rel. 11, Created)			
DT	01-JUL-1989 (Rel. 11, Last sequence update)			
DT	25-JAN-2005 (Rel. 46, Last annotation update)			
DE	Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-			
DE	associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)			
DE	(EPI).			
GN	Name=TFPI; Synonyms=LACI, TFPI1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RN	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=88198127; PubMed=2452157;			
RA	Wun T.-C., Kretzmer K.K., Girard T.J., Miletich J.P., Broze G.J. Jr.;			
RT	"Cloning and characterization of a cDNA coding for the lipoprotein-			
RT	associated coagulation inhibitor shows that it consists of three			
RT	tandem Kunitz-type inhibitory domains.";			
RL	J. Biol. Chem. 263:6001-6004(1988).			
RN	[2]			
RN	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=91129227; PubMed=1993173;			
RA	van der Logt C.P.E., Reitsma P.H., Bertina R.M.;			
RT	"Intron-exon organization of the human gene coding for the			
RT	lipoprotein-associated coagulation inhibitor: the factor Xa dependent			
RT	inhibitor of the extrinsic pathway of coagulation.";			
RL	Biochemistry 30:1571-1577(1991).			
RN	[3]			
RN	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=91161593; PubMed=2002045;			
RA	Girard T.J., Eddy R., Wesselschmidt R.L., Macphail L.A., Likert K.M.,			
RA	Byers M.G., Shows T.B., Broze G.J. Jr.;			
RT	"Structure of the human lipoprotein-associated coagulation inhibitor			
RT	gene. Intron/exon gene organization and localization of the gene to			
RT	chromosome 2.";			
RL	J. Biol. Chem. 266:5036-5041(1991).			
RN	[4]			
RN	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=89388722; PubMed=2781520; DOI=10.1016/0049-3848(89)90454-4;			
RA	Girard T.J., Warren L.A., Novotny W.F., Bejcek B.E., Miletich J.P.,			
RA	Broze G.J. Jr.;			
RT	"Identification of the 1.4 kb and 4.0 kb messages for the lipoprotein			
RT	associated coagulation inhibitor and expression of the encoded			
RT	protein.";			
RL	Thromb. Res. 55:37-50(1989).			
RN	[5]			
RN	SEQUENCE FROM N.A. (ISOFORM BETA).			
RP	Chang J.-Y., Monroe D.M., Roberts H.R.;			
RA	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.			
RL	[6]			

32	341	22.3	1572	2	O44938	haemochus
33	340	22.3	922	2	Q21418	caenorhabdi
34	337	22.1	1297	2	Q9N343	caenorhabdi
35	334.5	21.9	988	2	Q22685	caenorhabdi
36	332.5	21.8	1416	1	YN81_CABEL	caenorhabdi
37	327	21.4	1599	2	Q09983	caenorhabdi
38	314.5	20.6	142	2	Q8WPI2	boophilus m
39	309	20.2	1949	2	Q8MXG3	caenorhabdi
40	303.5	19.9	142	2	Q8WPI3	boophilus m
41	303	19.8	1391	2	Q19021	caenorhabdi
42	302.5	19.8	1743	2	Q9XWXS	caenorhabdi
43	296.5	19.4	1043	2	O17644	caenorhabdi
44	291	19.0	151	2	O6T269	bitis gabon
45	286.5	18.8	167	2	Q8NE89	homo sapien

RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,  
RA Ahearn M.O., Kuldane S.A., Rajkumar N., Toth E.J., Yi Q.,  
RA Nickerson D.A.;  
RT "SeattleSNPs, NHLBI HL6682 program for genomic applications, UW-  
RT FHCCRC, Seattle, WA (URL: <http://pga.gs.washington.edu/>).";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
RN [17]  
RP SEQUENCE FROM N.A. (ISOFORM BETA).  
RC TISSUE=Pancreas;  
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [8]  
RP SEQUENCE OF 29-50.  
RX MEDLINE=90036996; PubMed=2553722;  
RA Novotny W.F., Girard T.J., Miletich J.P., Broze G.J. Jr.;  
RT "Purification and characterization of the lipoprotein-associated  
RT coagulation inhibitor from human plasma.";  
RL J. Biol. Chem. 264:18832-18837 (1989).  
RN [9]  
RP SEQUENCE OF 29-43.  
RX PubMed=15340161; DOI=10.1110/ps.04682504;  
RA Zhang Z., Henzel W.J.;  
RT "Signal peptide prediction based on analysis of experimentally  
RT verified cleavage sites.";  
RL Protein Sci. 13:2819-2824 (2004).  
RN [10]  
RP INHIBITORY SITES.  
RX MEDLINE=89181950; PubMed=2927510; DOI=10.1038/338518a0;  
RA Girard T.J., Warren L.A., Novotny W.F., Likert K.M., Brown S.G.,  
RA Miletich J.P., Broze G.J. Jr.;  
RT "Functional significance of the Kunitz-type inhibitory domains of  
RT lipoprotein-associated coagulation inhibitor.";  
RL Nature 338:518-520 (1989).  
RN [11]  
RP CARBOHYDRATE-LINKAGE SITES.  
RX MEDLINE=96224851; PubMed=8639592; DOI=10.1021/bi9524880;  
RA Nakahara Y., Miyata T., Hamuro T., Funatsu A., Miyagi M.,  
RA Tsunawasa S., Kato H.;  
RT "Amino acid sequence and carbohydrate structure of a recombinant human  
RT tissue factor pathway inhibitor expressed in Chinese hamster ovary  
RT cells: one N- and two O-linked carbohydrate chains are located between  
RT Kunitz domains 2 and 3 and one N-linked carbohydrate chain is in  
RT Kunitz domain 2.";  
RL Biochemistry 35:6450-6459 (1996).  
RN [12]  
RP REVIEW.  
RX MEDLINE=91104709; PubMed=2271516;  
RA Broze G.J. Jr., Girard T.J., Novotny W.F.;  
RT "Regulation of coagulation by a multivalent Kunitz-type inhibitor.";  
RL Biochemistry 29:7539-7546 (1990).  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 121-178 IN COMPLEX WITH  
RP TRYPSIN.

RX MEDLINE=97390427; PubMed=9242660; DOI=10.1074/jbc.272.32.19931;  
RA Stubbs M.T., Morenweiser R., Stuerzebecher J., Bauer M., Bode W.,  
RA Huber R., Piechottka G.P., Matschner G., Sommerhoff C.P., Fritz H.,  
RA Auerswald E.A.;  
RT "The three-dimensional structure of recombinant leech-derived trypsinase  
RT inhibitor in complex with trypsin. Implications for the structure of  
RT human mast cell trypsinase and its inhibition.";  
RL J. Biol. Chem. 272:19931-19937 (1997).  
RN [14]  
RP STRUCTURE BY NMR OF 121-182.  
RX MEDLINE=97342711; PubMed=9199408; DOI=10.1006/jmbi.1997.1029;  
RA Burgerling M.J.M., Orbons L.P.M., van der Doelen A., Mulders J.,  
RA Theunissen H.J.M., Grootenhuys P.D.J., Bode W., Huber R., Stubbs M.T.;  
RT "The second Kunitz domain of human tissue factor pathway inhibitor:  
RT cloning, structure determination and interaction with factor Xa.";  
RL J. Mol. Biol. 269:395-407 (1997).  
RN [15]  
RP STRUCTURE BY NMR OF 210-270.  
RX PubMed=11772005; DOI=10.1021/bi011299g;  
RA Mine S., Yamazaki T., Miyata T., Hara S., Kato H.;  
RT "Structural mechanism for heparin-binding of the third Kunitz domain  
RT of human tissue factor pathway inhibitor.";  
RL Biochemistry 41:78-85 (2002).  
RN [16]  
RP VARIANT MET-292.  
RX MEDLINE=99318093; PubMed=10391209; DOI=10.1038/10290;  
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,  
RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.Q.,  
RA Lander E.S.;  
RT "Characterization of single-nucleotide polymorphisms in coding regions  
RT of human genes.";  
RL Nat. Genet. 22:231-238 (1999).  
RN [17]  
RP ERATUM.  
RX PubMed=10545957;  
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,  
RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.Q.,  
RA Lander E.S.;  
RL Nat. Genet. 23:373-373 (1999).  
CC -1- FUNCTION: Inhibits factor X (X(a)) directly and, in a Xa-dependent  
CC way, inhibits VIIa/tissue factor activity, presumably by forming a  
CC quaternary Xa/IACI/VIIa/TF complex. It possesses an antithrombotic  
CC action and also the ability to associate with lipoproteins in  
CC plasma.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Alpha; Synonyms=TFPIalpha;  
CC IsoId=P10646-1; Sequence=Displayed;  
CC Name=Beta; Synonyms=TFPIbeta;  
CC IsoId=P10646-2; Sequence=VSP\_003030, VSP\_003031;  
CC -1- TISSUE SPECIFICITY: Mostly in endothelial cells.  
CC -1- DOMAIN: This inhibitor contains three inhibitory domains. The  
CC first domain interacts with VIIa and TF, the second one with Xa.  
CC -1- PTM: O-glycosylated.  
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; J03225; AAA52022.1; -;  
CC EMBL; M58650; AAA59480.1; -;  
CC EMBL; M58644; AAA59480.1; JOINED.  
CC EMBL; M58645; AAA59480.1; JOINED.  
CC EMBL; M58646; AAA59480.1; JOINED.  
CC EMBL; M58647; AAA59480.1; JOINED.

```
DR EMBL; M58648; AAA59480.1; JOINED.
DR EMBL; M58649; AAA59480.1; JOINED.

Query Match
Best Local Similarity 100.0%; Score 1528; DB 1; Length 304;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTITDTLPLKLMHSCAFKADGPKAKMKRFFNIFTRQCEEFYGGCE 60
Db 29 DSEDEEHTITDTLPLKLMHSCAFKADGPKAKMKRFFNIFTRQCEEFYGGCE 88
Qy 61 GQNRFSLECKKCTRDNANRIKTTLOQEKDPFCFLEEDPGICRCGYITRYFYNNQTK 120
Db 89 GQNRFSLECKKCTRDNANRIKTTLOQEKDPFCFLEEDPGICRCGYITRYFYNNQTK 148
Qy 121 QCFERFKYGGCLGNMNNFETLBECKNICBDGPNQFVDNYGTQLNAVNNSLTPQSTKVPSL 180
Db 149 QCFERFKYGGCLGNMNNFETLBECKNICBDGPNQFVDNYGTQLNAVNNSLTPQSTKVPSP 208
Qy 181 FEHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSCGGNNFTSKQECRLACK 240
Db 209 FEHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSCGGNNFTSKQECRLACK 268
Qy 241 KGFTQRIKSGGLIKTKRKRKQKVIAEYEFVKNM 276
Db 269 KGFTQRIKSGGLIKTKRKRKQKVIAEYEFVKNM 304

RESULT 2
TFPI_MACMU
ID TFPI_MACMU STANDARD; PRT; 304 AA.
AC Q28864;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
DE associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
DE (EPI).
GN Name=TFPI; Synonyms=TFPI1;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94375417; PubMed=8089087;
RA Kamei S., Kanikubo Y., Hamuro T., Fujimoto H., Ishihara M.,
RA Yonemura H., Miyamoto S., Funatsu A., Enjiyoji K., Abumiya T.;
RT "Amino acid sequence and inhibitory activity of rhesus monkey tissue
RT factor pathway inhibitor (TFPI): comparison with human TFPI.";
RL J. Biochem. 115:708-714(1994).
CC -!- FUNCTION: Inhibits factor X (X(a)) directly and, in a Xa-dependent
CC way, inhibits VIIa/tissue factor activity, presumably by forming a
CC quaternary Xa/LACI/VIIa/TF complex. It possesses an antithrombotic
CC action and also the ability to associate with lipoproteins in
CC plasma.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: This inhibitor contains three inhibitory domains. The
CC first domain interacts with VIIa and TF, the second one with Xa
CC (By similarity).
CC -!- PTM: O-glycosylated (By similarity).
CC -!- SIMILARITY: Contains 3 BPRI/Kunitz inhibitor domains.
CC -----
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CC -----

EMBL; S73337; AAB31955.1; -.
PIR; JC2264; JC2264.
HSP; P10646; IIRH.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008296; TFPI.
PFam; PF00014; Kunitz BPRI; 3.
DR PIRSF; PIRSF001620; TFPI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 3.
KW Blood coagulation; Glycoprotein; Repeat; Serine protease inhibitor;
KW Signal.
FT SIGNAL 1 28 By similarity.
FT CHAIN 29 304 Tissue factor pathway inhibitor.
FT DOMAIN 54 104 BPTI/Kunitz inhibitor 1.
FT DOMAIN 125 175 BPTI/Kunitz inhibitor 2.
FT DOMAIN 217 267 BPTI/Kunitz inhibitor 3.
FT SITE 64 65 Reactive bond (By similarity).
FT SITE 135 136 Reactive bond (By similarity).
FT SITE 227 228 Reactive bond (By similarity).
FT DISULFID 54 104 By similarity.
FT DISULFID 63 87 By similarity.
FT DISULFID 79 100 By similarity.
FT DISULFID 125 175 By similarity.
FT DISULFID 134 158 By similarity.
FT DISULFID 150 171 By similarity.
FT DISULFID 217 267 By similarity.
FT DISULFID 226 250 By similarity.
FT DISULFID 242 263 By similarity.
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 195 195 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 256 256 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 304 AA; 35085 MW; 56E13B3FF16282B0 CRC64;

Query Match
Best Local Similarity 94.7%; Score 1447; DB 1; Length 304;
Matches 259; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DSEDEEHTITDTLPLKLMHSCAFKADGPKAKMKRFFNIFTRQCEEFYGGCE 60
Db 29 DSEDEEHTITDTLPLKLMHSCAFKADGPKAKMKRFFNIFTRQCEEFYGGCE 88
Qy 61 GQNRFSLECKKCTRDNANRIKTTLOQEKDPFCFLEEDPGICRCGYITRYFYNNQTK 120
Db 89 GQNRFSLECKKCTRDNANRIKTTLOQEKDPFCFLEEDPGICRCGYITRYFYNNQTK 148
Qy 121 QCFERFKYGGCLGNMNNFETLBECKNICBDGPNQFVDNYGTQLNAVNNSLTPQSTKVPSL 180
Db 149 QCFERFKYGGCLGNMNNFETLBECKNICBDGPNQFVDNYGTQLNAVNNSLTPQSTKVPSP 208
Qy 181 FEHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSCGGNNFTSKQECRLACK 240
Db 209 FEHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSCGGNNFTSKQECRLACK 268
Qy 241 KGFTQRIKSGGLIKTKRKRKQKVIAEYEFVKNM 276
Db 269 KGFTQRIKSGGLIKTKRKRKQKVIAEYEFVKNM 304

RESULT 3
TFPI_RABIT
ID TFPI_RABIT STANDARD; PRT; 300 AA.
AC P19761; Q28828;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 23, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
DE associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
DE (EPI).
GN Name=TFPI;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
NCBI\_TaxID=9986;  
[1]  
SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=91057146; PubMed=2136251;  
RA Wesselschmidt R.L., Girard T.J., Broze G.J. Jr.;  
RT "cDNA sequence of rabbit lipoprotein-associated coagulation  
inhibitor.";  
RL Nucleic Acids Res. 18:6440-6440(1990).  
[2]  
REVIEWS TO 72; 211 AND 218.  
RC TISSUE=Liver;  
RX MEDLINE=92335027; PubMed=1630940;  
RA Warn-Cramer B.J., Broze G.J. Jr., Komives E.A.;  
RT "cDNA sequence of rabbit tissue factor pathway inhibitor.";  
RL Nucleic Acids Res. 20:3548-3548(1992).  
[3]  
SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=93276427; PubMed=9503123; DOI=10.1016/0049-3848(93)90059-W;  
RA Belaaouaj A., Kuppussawmy M.N., Birkcoft J.U., Bajaj S.P.;  
RT "Revised cDNA sequence of rabbit tissue factor pathway inhibitor.";  
RL Thromb. Res. 69:547-553(1993).  
CC -1- FUNCTION: Inhibits factor X (X(a)) directly and, in a Xa-dependent  
way, inhibits VIIa/tissue factor activity, presumably by forming a  
quaternary Xa/LACI/VIIa/TF complex. It possesses an antithrombotic  
action and also the ability to associate with lipoproteins in  
plasma.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- DOMAIN: This inhibitor contains three inhibitory domains. The  
first domain interacts with VIIa and TF, the second one with Xa  
(By similarity).  
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR EMBL; X54708; CAA38515.1; ALT\_SEQ.  
DR EMBL; S61902; AAB26836.1; -.  
DR PIR; I46937; I46937.  
DR HSSP; P10646; ITFX.  
DR InterPro; IPR002223; Prot\_Inh\_Kunz-m.  
DR InterPro; IPR008296; TFPI.  
DR Pfam; PF00004; Kunitz\_BPTI; 3.  
DR PIRSF; PIRSF001620; TFPI; 1.  
DR PRINTS; PR00759; BASICPTASE.  
DR PRODOM; PD000222; Prot\_Inh\_Kunz-m; 3.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 3.  
DR PROSITE; PS02079; BPTI\_KUNITZ\_2; 3.  
KW Blood coagulation; Glycoprotein; Repeat; Serine protease inhibitor;  
KW Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 300 Tissue factor pathway inhibitor.  
FT DOMAIN 50 100 BPTI/Kunitz inhibitor 1.  
FT DOMAIN 121 171 BPTI/Kunitz inhibitor 2.  
FT DOMAIN 213 263 BPTI/Kunitz inhibitor 3.  
FT SITE 60 61  
FT SITE 131 132 Reactive bond (By similarity).  
FT SITE 223 224 Reactive bond (By similarity).  
FT SITE 225 226 By similarity.  
FT DISULFID 59 83 By similarity.  
FT DISULFID 75 96 By similarity.  
FT DISULFID 121 171 By similarity.  
FT DISULFID 130 154 By similarity.  
FT DISULFID 146 167 By similarity.  
FT DISULFID 213 263 By similarity.  
FT DISULFID 222 246 By similarity.











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DR InterPro: IPR008296; TPPI.
DR Pfam: PF00014; Kunitz_BPTI; 3.
DR PIRSF: PIRSF001620; TFI; 1.
DR PRINTS: PR00759; BASICPASS.
DR PRODOM: PD000222; Prot_Inh_Kunz-m; 3.
DR SMART: SM00131; KU; 3.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE: PS02079; BPTI_KUNITZ_2; 3.
KW Hypothetical protein.
SQ SEQUENCE 287 AA; 33093 MW; DF69B3D76718115E CRC64;

Query Match 33.9%; Score 518; DB 2; Length 287;
Best Local Similarity 36.6%; Pred. No. 1.1e-35;
Matches 97; Conservative 48; Mismatches 78; Indels 42; Gaps 5;

Qy 19 LKLMHSCAFKADGPKAKMKRFFNFTQCEEFYGGCGNQRNFESLECKKMC 78
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 35 ITHFHSKALKKDEGPKALKDRFYDFTDTCESFEYGGCGNQRNFETLQCEKMC - 92
Qy 79 DNANRIKTTLOQEKDFCFLEEDPGICRGVITRYFYNNQTKQCFKYGCGCLGNMNF 138
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 93 -----LVKEDKSPCLDDEPGCRGLVPYFFDFKQCEKRFYGGCGFNANFK 142
Qy 139 TLECKNICEDGPNQFQ-----VDNYGTQLNAV-----NSLTPOSTK 176
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 143 TIKECHERCLPALNNMERNAPLKEEBAKPKTEPLAKHVEAPLNASHLPQKSKPSAK 202
Qy 177 VPSLFEHFGPSWCLTPADRGICRANENRFFYNSVIGKCRPFYGGCGNQRNFESLECK 236
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 203 KPLR---NRPKLFCSPIDGNCSEGRYMYNPRTKRCQMFHYSGCGNKNFVKRGDCI 259
Qy 237 RACKGFGTQRIKSGGLIKTKRK 261
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 260 KCMRDLRRK-----LIRLKLRSK 279

RESULT 11
Q7T025 PRELIMINARY; PRT; 224 AA.
ID Q7T025 PRELIMINARY; PRT; 224 AA.
AC Q7T025;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC68843 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Alcega S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
```

```

[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391 (2002).
[3]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; BC055972; AAH55972.1; -.
DR HSSP; P00974; 1BPI.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 3.
SQ SEQUENCE 224 AA; 25538 MW; 11C2D1C4C789445B CRC64;

Query Match 30.3%; Score 463; DB 2; Length 224;
Best Local Similarity 36.5%; Pred. No. 3.7e-31;
Matches 91; Conservative 34; Mismatches 68; Indels 56; Gaps 6;

Qy 18 PLKLMHSCAFKADGPKAKMKRFFNFTQCEEFYGGCGNQRNFESLECKKMC 77
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 22 PMQNTTVCLLPLDEGPKALIPHYDYDTQCEFFYGGCGNQRNFESLECKKMC 81
Qy 78 RDANRIKTTLOQEKDFCFLEEDPGICRGVITRYFYNNQTKQCFKYGCGCLGNMNF 137
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 82 K-----LK-----KVPKACRMVDEGFCRGYIKRYANMKTMRCEQFIYGGCGNDRNF 130
Qy 138 ETLCKNICEDGPNQFQVDNYGTQLNAVNSLTPOSTKVPSPSLFEHFGPSWCLTPADRG 197
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 131 QDKDCINFC-----APRR-----DAPSPCYSPKDEGS 158
Qy 198 CRANENRFFYNSVIGKCRPFYGGCGNQRNFESLECKKMC 257
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 159 CSASVTTRYFYFNIESKACEEFYTCGCGNSNNFIKVEDCDSCYCKKG-----TKR 206
Qy 258 KRKKQKRVKI 266
Dy 207 PR-NQNPKI 214

RESULT 12
Q8AVE1 PRELIMINARY; PRT; 277 AA.
ID Q8AVE1 PRELIMINARY; PRT; 277 AA.
AC Q8AVE1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tissue factor pathway inhibitor.
GN Name:tfpia;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1]
RP SEQUENCE FROM N.A.
RA Hanumanthaiah R., Day K., Jagadeeswaran P.;
RT "Comprehensive analysis of blood coagulation pathways in teleostei:
Evolution of coagulation factor genes and identification of zebrafish
factor VIII.";
RL Blood Cells Mol. Dis. 0:0-0 (2002).
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
```

DR	EMBL; AF515274; AAN71004.1; -.
DR	HSSP; P31713; 1SPH.
DR	ZFIN; ZDB-GENE-030711-1; tfpia.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0030414; F:protease inhibitor activity; IEA.
DR	GO; GO:0004867; F:sarime-type endopeptidase inhibitor activity; IEA.
DR	GO; GO:0007936; P:blood coagulation; IEA.
DR	InferPro; IPR002223; Prot_Inh_Kunz-m.
DR	InferPro; IPR008296; TPFI.
DR	Pfam; PF00014; Kunitz_BPTI; 3.
DR	PIRSF; PIRSF001620; TPFI; 1.
DR	PRINTS; PR00759; BASICPTASE.
DR	ProDom; PD000222; Prot_Inh_Kunz-m; 3.
DR	SMART; SM00131; KU; 2.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR	PROSITE; PS00279; BPTI_KUNITZ_2; 2.
SQ	SEQUENCE 277 AA; 31942 MW; 0F68FOEAFF9B100F CRC64;

  

Query Match	29.2%; Score 446; DB 2; Length 277;
Best Local Similarity	31.4%; Pred. No. 1.3e-29;
Matches	86; Conservative 58; Mismatches 84; Indels 46; Gaps 5;

  

Qy	19 LKLMHSFCAFKADGPKCAIMKRFFNFTROCEEFYGGCGEGNONRFESELECKMKCTR 78
Dd	34 LRIPHQSALRKDEGPCAKMDRYFDIDTCRCPEFYGGCGGNANFETIQDCEMC-- 91
Qy	79 DNANRIKTTLQOBKPDPCFLEEDPGICRGYITRFYNNTQKOCERKYGGCLGNMNF 138
Dd	92 -----LVTENKSPCHLEDPEGPCRGLVPRYFFDQKSQECKPFYGGCFGANNFK 141
Qy	139 TLECKNICE-----DGPNGFQVDNYGTQLNAVNNSLTPOSTKVPSLFE 182
Dd	142 TIKACQQRCLTAVLKSEEEAKPVIESP----AIHDDAHLNSSHLSALSRVPQAKOEA 197
Qy	183 FHGPSWCLTPADRGLCRANENRFYNSVI GKRCFPKYGGCGGNNNFTSKOECLRACKG 242
Dd	198 FSPPELCMSAVDRGCDGSERYVFNRI GECQVFR-SLDVEEQKLHPQHCMKC--- 253
Qy	243 FIORISKGGLIKTRKKRKKORVKIAYEEIFVMNM 276
Dd	254 -----MKDQHRKQRIKRTNSNILFRSV 277

RESULT 13	
Q8IT91	
ID	PRELIMINARY; PRT; 759 AA.
QC	Q8IT91
AC	Q8IT91;
DT	01-MAR-2003 (TrEMBLrel. 23, Created)
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Kunitz-like protease inhibitor precursor.
DE	Ancyllostoma caninum (Dog hookworm).
OS	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC	Ancyllostomatodea; Ancyllostomatidae; Ancylostomatinae; Ancylostoma.
OX	NCBI_TaxID=29170;
ON	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Baltimore;
RY	MEDLINE=22645137; PubMed=12760667;
RT	Rawdon J.M., Datu B., Crowell M.;
RT	"Molecular cloning of a novel multidomain Kunitz-type proteinase
RL	inhibitor from the hookworm Ancylostoma caninum.";
RL	J. Parasitol. 89:402-407(2003).
CC	-/- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR	EMBL; AF533590; AAN10061.1; -.
DR	HSSP; P31713; LSHP.
DR	GO; GO:0008233; F:peptidase activity; IEA.
DR	GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR	InterPro; IPR002223; ProtInh_Kunz-m.
DR	Pfam; PF00014; Kunitz_BPTI; 12.
DR	PRINTS; PR00759; BASICTPASE.
DR	SMART; SM00131; KU; 12.
DR	PROSITE; PS00280; BPTI_KUNITZ 1; 10.

```

DR PROSITE; PS50279; BPTI_KUNITZ_2; 12.
KW Protease; Signal.
FT SIGNAL 1 16 Potential.
SQ SEQUENCE 759 AA; 84886 MW; C431A3C3F418F40A CRC64;

Query Match 27.1%; Score 414.5; DB 2; Length 759;
Best Local Similarity 33.6%; Pred. No. 1.9e-26;
Matches 97; Conservative 33; Mismatches 106; Indels 53; Gaps 6;

QY 3 EEDDEHTIITDTELPPLKLMHSCAFKADQDPCKAIMKRFFFTFTQCEFIYGGCGEN 62
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 370 ESMEECTRTCKAVPEPEPEKETCSQPIEVGPKAMLKRYAYDNKKKCVRFIYGGCKGN 429
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 63 QNRFESLECKMCKTRDNRANRIKTHLOQKPDPCFLEEDPGICRGYITRYFYNNQTKQC 122
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 430 KNNFESMEECTRTCT-----KKAVPEPEQDTCSPQIEVGPCKAMLKRYAYDNKKKNC 480
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 123 ERFKYGGCLGNMNFLETSEKNIC-----EDGP-----NGFQVDN- 158
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 481 VRFIYGGCKGNKNFESMEECTRTCKKAVPEPEPEKETCSQPIEAGPKAWRRFAYDNA 540
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 159 -----YGTQLMANVNSLT-----PQSTKVPSLFEFHGPSWCLTTPADRLCLRANE 202
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 541 KEKCVPEFFYGGCKGNKKNFETMEDCTFTCQRLAKEPLEK----DVCSPQITAGPCRASI 596
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 203 NRFYNSVIQKRPFKYGGCGNNENNTSKQECCLRACKGFIORISGG 251
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 597 PRYGYDSKKRKKVKFTYGGCKGNRFPPTKNECEKTKRGATGTTNPGG 645
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
QYRQ8 PRELIMINARY; PRT; 234 AA.
AC QYRQ8
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Tissue factor pathway inhibitor-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI TaxID=9913;

```

## RESULT 14

Q7YRQ8	PRELIMINARY;	PRT;	234 AA.
ID	QYVRQ8		
AC	QYVRQ8		
DT	01-OCT-2003 (T-EMBLrel. 25, Created)		
DT	01-OCT-2003 (T-EMBLrel. 25, Last sequence update)		
DT	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)		
DE	Tissue factor pathway inhibitor-2.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22802738; PubMed=12921785; DOI=10.1016/S0003-9861(03)00332-1;		
RA	Du X., Deng F.M., Chand H.S., Kisiel W.;		
RT	"Molecular cloning, expression, and characterization of bovine tissue		
RT	factor pathway inhibitor-2".		
RL	Arch. Biochem. Biophys. 417:96-104 (2003).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Deng F.-M., Kisiel W., Sun T.-T.;		
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.		
DR	EMBL; AY234861; RA084035.1; -.		
DR	HSPSP; P00981; IDTK.		
DR	GO; GO:0004967; F.Serine-type endopeptidase inhibitor activity; IEA.		
DR	InterPro; IPR002223; Prot Inh Kunz-m.		
DR	Pfam; PFO0014; Kunitz BPTI; 3-		
DR	ProDom; PD000222; Prot_Inh_Kunz-m; 3.		
DR	SMART; SM00131; KU; 3.		
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 3.		
DR	PROSITE; PS02079; BPTI_KUNITZ_2; 3.		
SQ	SEQUENCE 234 AA; 26675 MW; 401EEC84D589B422 CRC64;		

		Query Match	25.7%	Score 392;	DB 2:	Length 234;
		Best Local Similarity	29.3%;	Pred. NO. 3.9e-35;		
		Matches	78;	Conservative 41;	Mismatches 93;	Indels 54; Gaps 4;
QY	9	TIIITDLPPLKLMISFCFAFKADGGCKATMKRFFNNIFTRQCEEFYIGCGEGNONRFES	68			
Dd	19	TALGDASAPPNGNATICLLPPDDGRCARIPSYVDRYTQSFRFYMGCEGNANNFET	78			



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2005, 03:17:23 ; Search time 44 Seconds  
(without alignments)  
603.542 Million cell updates/sec

Title: US-10-753-079-1

Perfect score: 1528

Sequence: 1 DSEDEDEHTIITDTELPPLK.....RRKKQKRVKIAYEIEIFVKNM 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1528	100.0	304	1	TIHUGK
2	1447	94.7	304	1	JC2264
3	1124	73.6	299	2	I46937
4	1112	72.8	300	2	S12143
5	993	65.0	396	2	S53325
6	934.5	61.2	302	1	TIRTKK
7	384.5	25.2	235	2	A54951
8	355.5	23.3	1558	2	C89114
9	355.5	23.3	2167	2	T34395
10	350.5	22.9	2225	2	T26063
11	347	22.7	1474	2	D88550
12	340	22.3	922	2	T23573
13	334.5	21.9	1522	2	H88380
14	332.5	21.8	1416	2	B88550
15	332.5	21.8	2844	2	S28291
16	327	21.4	1599	2	T16210
17	309	20.2	1965	2	T33216
18	303	19.8	1391	2	T20406
19	302.5	19.8	1743	2	T26859
20	296.5	19.4	1043	2	T19734
21	253	16.6	838	2	T20125
22	252.5	16.5	1203	1	T21275
23	240.5	15.7	352	1	HCHU
24	239	15.6	125	1	TIHOB1
25	238	15.6	123	2	A29652
26	236	15.4	252	2	JG0185
27	233	15.2	1208	2	T27822
28	232.5	15.2	352	1	TIHOB1
29	229	15.0	337	1	TIIPGB1

30	225.5	14.8	349	2	S21089	alpha-1-microglobu
31	223	14.6	349	2	S35708	alpha-1-microglobu
32	220.5	14.4	692	2	T32980	hypothetical prote
33	199	13.0	372	2	JC2556	alpha-1-microglobu
34	196.5	12.9	355	1	S22181	gamma-1-microglobu
35	190.5	12.5	805	2	T34212	hypothetical prote
36	189.5	12.4	183	2	T28711	hypothetical prote
37	189	12.4	65	1	TIIVVC	venom basic protei
38	183	12.0	61	1	TIIVTI	venom basic protei
39	183	12.0	62	2	S19327	venom basic protei
40	176	11.5	62	2	A44180	taicatoxin serine
41	175.5	11.5	110	1	TIITOR	basic proteinase i
42	172	11.3	67	1	TIBOC	trypsin inhibitor,
43	170	11.1	219	2	T21736	hypothetical prote
44	169	11.1	58	1	TIHABK	isoinhibitor K (BP
45	169	11.1	60	1	TIIVRV2	venom basic protei

#### ALIGNMENTS

#### RESULT 1

TIHUGK

tissue factor pathway inhibitor precursor [validated] - human

N:Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004

C:Accession: A23712; A39176; A28650; A60433; B60433; S13034; A34315; A38294; S03903

R:Girard, T.J.; Eddy, R.; Wesselschmidt, R.L.; MacPhail, L.A.; Likert, K.M.; Byers, M.G.  
J. Biol. Chem. 266, 5036-5041, 1991

A:Title: Structure of the human lipoprotein-associated coagulation inhibitor gene. Intro

A:Reference number: A23712; MUID:91161593; PMID:2002045

A:Accession: A23712

A:Molecule type: DNA

A:Residues: 1-304 <GIR>

A:Cross-references: UNIPROT:P10646; GB:M59493; GB:M59499; NID:g187204; PIDN:AAA59536.1;

R:van der Logt, C.P.E.; Reitsma, P.H.; Bertina, R.M.

Biochemistry 30, 1571-1577, 1991

A:Title: Intron-exon organization of the human gene coding for the lipoprotein-associated

A:Reference number: A39176; MUID:91129227; PMID:1993173

A:Accession: A39176

A:Molecule type: DNA

A:Residues: 1-304 <VAN>

A:Cross-references: GB:M58650; GB:J05312; NID:g186827; PIDN:AAA59480.1; PID:g186829

R:Wun, T.C.; Kretzmer, K.K.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.

J. Biol. Chem. 263, 6001-6004, 1988

A:Title: Cloning and characterization of a cDNA coding for the lipoprotein-associated co

A:Reference number: A28650; MUID:88198127; PMID:2452157

A:Accession: A28650

A:Molecule type: mRNA

A:Residues: 1-304 <WUN>

A:Cross-references: GB:J03225; NID:g180545; PIDN:AAA52022.1; PID:g180546

A:Note: part of this sequence, including the amino end of the mature protein, was confil

R:Girard, T.J.; Warren, L.A.; Novotny, W.F.; Bejcek, B.E.; Miletich, J.P.; Broze Jr., G.

Thromb. Res. 55, 37-50, 1989

A:Title: Identification of the 1.4 KB and 4.0 KB messages for the lipoprotein associated

A:Reference number: A60433; MUID:89388722; PMID:2781520

A:Accession: A60433

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-304 <GI2>

A:Experimental source: endothelial cells

A:Accession: B60433

A:Molecule type: protein

A:Residues: 'XX', 31-53, 'X', 55-56 <GI3>

A:Experimental source: recombinant material from mouse C137 cells

R:Girard, T.J.; McCourt, D.; Novotny, W.F.; MacPhail, L.A.; Likert, K.M.; Broze Jr., G.J.

Biochem. J. 270, 621-625, 1990

A:Title: Endogenous phosphorylation of the lipoprotein-associated coagulation inhibitor

A:Reference number: S13034; MUID:91054349; PMID:2122883

A:Accession: S13034

A:Molecule type: protein

A:Residues: 29-35 <GI4>

R;Novotny, W.F.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.  
J. Biol. Chem. 264, 18832-18837, 1989  
A;Title: Purification and characterization of the lipoprotein-associated coagulation inhibitor  
A;Reference number: A34315; MUID:90036996; PMID:2553722  
A;Accession: A34315  
A;Molecule type: protein  
A;Residues: 'XX', 31-33, 'L', 35-50 <NOV>  
A;Experimental source: plasma  
R;Pedersen, A.H.; Nordfang, O.; Norris, F.; Wiberg, F.C.; Christensen, P.M.; Moeller, K.  
J. Biol. Chem. 265, 16786-16793, 1990  
A;Title: Recombinant human extrinsic pathway inhibitor. Production, isolation, and characterization  
A;Reference number: A38294; MUID:91009092; PMID:2211593  
A;Accession: A38294  
A;Molecule type: protein  
A;Residues: 29-41 <PED>  
R;Girard, T.J.; Warren, L.A.; Novotny, W.F.; Likert, K.M.; Brown, S.G.; Miletich, J.P.; Nature 338, 518-520, 1989  
A;Title: Functional significance of the Kunitz-type inhibitory domains of lipoproteinase-A  
A;Reference number: S03903; MUID:89181950; PMID:2927510  
A;Contents: annotation; site-directed mutagenesis  
C;Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the  
C;Genetics:  
A;Gene: GDB:TFPI  
A;Cross-references: GDB:127364; OMIM:152310  
A;Map position: 2q32-2q32  
A;Introns: 41/1; 107/1; 120/1; 179/1; 210/1; 270/1  
C;Function:  
A;Description: regulates clotting by factor Xa-dependent inhibition of the coagulation factor  
A;Pathway: blood coagulation  
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor  
C;Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding  
F;1-28/Domain: signal sequence #status predicted <SIG>  
F;29-304/Product: tissue factor pathway inhibitor #status experimental <MAT>  
F;54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>  
F;217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>  
F;54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>  
F;54-104, 63-87, 79-100, 125-175, 134-158, 150-171, 217-267, 226-250, 242-263/Disulfide bonds: #  
F;64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predicted  
F;135/Inhibitory site: Arg (coagulation factor X) #status predicted  
F;145, 195, 256/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;227/Inhibitory site: Arg (unidentified proteinase) #status predicted  
Query Match 100.0%; Score 1528; DB 1; Length 304;  
Best Local Similarity 100.0%; Pred. No. 8.8e-118;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DSEDEEHTIITDELPLKLMHSFCAPKADGCKAIMKRFNFTTQCEEFYGGCE 60  
Db 29 DSEDEEHTIITDELPLKLMHSFCAPKADGCKAIMKRFNFTTQCEEFYGGCE 88  
Qy 61 GNQRFSLSECKKMCNTRDANRIKTTLOQKDFCFLEDPGICRGYITRYFNNQTK 120  
Db 89 GNQRFSLSECKKMCNTRDANRIKTTLOQKDFCFLEDPGICRGYITRYFNNQTK 148  
Qy 121 QCFERFKYGGCLGNMNNFETLECKNICEDGPNQGVNDYGTQLNANNSLTTPQSTKVPSSL 180  
Db 149 QCFERFKYGGCLGNMNNFETLECKNICEDGPNQGVNDYGTQLNANNSLTTPQSTKVPSSL 208  
Qy 181 FEHGPSWCLTPADRGICLANENRFFYNSVIGKCRPPKYSKCGGNNFTSKQBLRACK 240  
Db 209 FEHGPSWCLTPADRGICLANENRFFYNSVIGKCRPPKYSKCGGNNFTSKQBLRACK 268  
Qy 241 KGFIQRISKGLIKTKRKKQKRVKIAVEEFVKNM 276  
Db 269 KGFIQRISKGLIKTKRKKQKRVKIAVEEFVKNM 304  
RESULT 2  
JC2264  
tissue factor pathway inhibitor precursor - rhesus macaque  
N;Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib

C;Species: Macaca mulatta (rhesus macaque)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: JC2264  
R;Kamei, S.; Kamikubo, Y.; Hamuro, T.; Fujimoto, H.; Ishihara, M.; Yonemura, H.; Miyamoto, J. Biochem. 115, 708-714, 1994  
A;Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor pathway inhibitor  
A;Reference number: JC2264; MUID:94375417; PMID:8089087  
A;Accession: JC2264  
A;Molecule type: mRNA  
A;Residues: 1-304 <KAM>  
A;Cross-references: UNIPROT:Q28864; GB:S73337; NID:G685016; PIDN:AAB31955.1; PID:G685017  
A;Experimental source: liver  
C;Comment: This protein inhibits the activities of factor Xa and tissue factor-VI  
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor  
C;Keywords: anticoagulant; glycoprotein; serine proteinase inhibitor  
F;1-28/Domain: signal sequence #status predicted <SIG>  
F;29-304/Product: tissue factor pathway inhibitor #status predicted <MAT>  
F;54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>  
F;217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>  
F;54-104, 63-87, 79-100, 125-175, 134-158, 150-171, 217-267, 226-250, 242-263/Disulfide bonds: #  
F;64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predicted  
F;135/Inhibitory site: Arg (coagulation factor X) #status predicted  
F;145, 195, 256/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;227/Inhibitory site: Arg (unidentified proteinase) #status predicted  
Query Match 94.7%; Score 1447; DB 1; Length 304;  
Best Local Similarity 93.8%; Pred. No. 3.8e-111;  
Matches 259; Conservative 8; Mismatches 9; Indels 0; Gaps 0;  
Qy 1 DSEDEEHTIITDELPLKLMHSFCAPKADGCKAIMKRFNFTTQCEEFYGGCE 60  
Db 29 DSEDEEHTIITDELPLKLMHSFCAPKADGCKAIMKRFNFTTQCEEFYGGCE 88  
Qy 61 GNQRFSLSECKKMCNTRDANRIKTTLOQKDFCFLEDPGICRGYITRYFNNQTK 120  
Db 89 GNQRFSLSECKKMCNTRDANRIKTTLOQKDFCFLEDPGICRGYITRYFNNQTK 148  
Qy 121 QCFERFKYGGCLGNMNNFETLECKNICEDGPNQGVNDYGTQLNANNSLTTPQSTKVPSSL 180  
Db 149 QCFERFKYGGCLGNMNNFETLECKNICEDGPNQGVNDYGTQLNANNSLTTPQSTKVPSSL 208  
Qy 181 FEHGPSWCLTPADRGICLANENRFFYNSVIGKCRPPKYSKCGGNNFTSKQBLRACK 240  
Db 209 FEHGPSWCLTPADRGICLANENRFFYNSVIGKCRPPKYSKCGGNNFTSKQBLRACK 268  
Qy 241 KGFIQRISKGLIKTKRKKQKRVKIAVEEFVKNM 276  
Db 269 KGFIQRISKGLIKTKRKKQKRVKIAVEEFVKNM 304  
RESULT 3  
I46937  
tissue factor pathway inhibitor - rabbit  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 09-Jul-2004  
C;Accession: I46937  
R;Belasouaj, A.; Kuppaswamy, M.N.; Birktoft, J.J.; Bajaj, S.P. Thromb. Res. 69, 547-553, 1993  
A;Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.  
A;Reference number: I46937; MUID:93276427; PMID:8503123  
A;Accession: I46937  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-299 <BEL>  
A;Cross-references: UNIPROT:P19761; GB:S61902; NID:G386015; PIDN:AAB26836.1; PID:G386016  
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor  
F;49-99/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
F;120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
F;212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>  
Query Match 73.6%; Score 1124; DB 2; Length 299;  
Best Local Similarity 73.4%; Pred. No. 1e-84;



C:Comment: This serine proteinase inhibitor regulates clotting by factor Xa-dependent in  
C:Superfamily: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the  
C:Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-302/Product: tissue factor pathway inhibitor #status predicted <MAT>  
F:53-103/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
F:124-174/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>  
F:222-272/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>  
F:288-291/Region: heparin binding #status predicted  
F:53-103,62-86,78-99,124-174,133-157,149-170,222-272,231-255,247-269/Disulfide bonds: #s  
F:63/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predicted  
F:134/Inhibitory site: Arg (coagulation factor VII) #status predicted  
F:144,251,261/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:232/Inhibitory site: Lys (unidentified proteinase) #status predicted

Query Match 61.2%; Score 934.5; DB 1; Length 302;  
Best Local Similarity 60.9%; Pred. No. 3.5e-69;  
Matches 167; Conservative 40; Mismatches 58; Indels 9; Gaps 3;

Qy 4 EDEHTITDTELPPLKLMHSFCFAKDDGPKCKAIMKRFNFNITROCEEFYGGCEGNO 63  
Db 31 EEDDTINTSELPKPLHIFCAKADGPKAMIRSYIFNMHSQCSEEFYGGCEGNO 90

Qy 64 NRPFSLECKKMTDNRANRIKTLQOEKDFCFLEDPGICRGYITRYFNNQTKQE 123  
Db 91 NRPFTLECRKTCIPGYKTKITKTSAGKDFCFLEDPGICRGYITRYFNNQTKQE 150

Qy 124 RPKYGGCLGNMNFETLECKNICEGDPNGQVDNY-----GTQLNAVNNLSLPQSTKV 177  
Db 151 QPKYGGCLGNMNFETLECKNICEGDPNGQVDNY-----GTQLNAVNNLSLPQSTKV 210

Qy 178 PSLFEFGHPSWCLPADRGCLCRANENRYNSVLGKCRPFYSGCGNENFTSKOECLR 237  
Db 211 PSQWDYDGPWCLPFAUSGLCKAEKRYNPALCKRQFYNTGCGNNNFTTKQDCNR 270

Qy 238 ACKGFTQIRISKGLIKTKRKQKQKVIAYEEI 271  
Db 271 ACKDSSKSKSRA--KTQR--RRKSFVKVMYENI 301

RESULT 7  
A:54951  
tissue factor pathway inhibitor-2 precursor - human  
N:Alternate names: placental protein 5 (pps)  
C:Species: Homo sapiens (man)  
C:Date: 31-May-1996 #sequence revision 31-May-1996 #text\_change 09-Jul-2004  
C:Accession: A54951; I55185; A34029; B34029  
R:Spracher, C.A.; Kiesel, W.; Mathewes, S.; Foster, D.C.  
Proc. Natl. Acad. Sci. U.S.A. 91, 3353-3357, 1994  
A:Title: Molecular cloning, expression, and partial characterization of a second human t  
A:Reference number: A54951; MUID:94211862; PMID:8159751  
A:Accession: A54951  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-235 <RES>  
A:Cross-references: UNIPROT:P48307; GB:L27624; NID:g441149; PIDN:AAA20094.1; PID:g441150  
A:Experimental source: placenta  
R:Miyagi, Y.; Koshikawa, N.; Yasumitsu, H.; Miyagi, E.; Hirahara, F.; Aoki, I.; Misugi,  
J. Biochem. 116, 339-942, 1994  
A:Title: cDNA cloning and mRNA expression of a serine proteinase inhibitor secreted by c  
A:Reference number: I55185; MUID:95204397; PMID:7896752  
A:Accession: I55185  
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME  
A:Molecule type: mRNA  
A:Residues: 1-235 <R2>  
A:Cross-references: GB:D29992; NID:g484050; PIDN:BAA06272.1; PID:g484051  
A:Note: parts of this sequence, including the amino end of the mature protein, were dete  
R:Butzow, R.; Huhtala, M.L.; Bohn, H.; Virtanen, I.; Seppälä, M.  
Biochem. Biophys. Res. Commun. 150, 483-490, 1988  
A:Title: Purification and characterization of placental protein 5.  
A:Reference number: A34029; MUID:88106628; PMID:3276312  
A:Accession: A34029

A:Molecule type: protein  
A:Residues: 'A',24-33,'X',35 <BUE>  
A:Accession: C34029  
A:Molecule type: protein  
A:Residues: 47-50,'X',52-53 <BU2>  
A:Accession: B34029  
A:Molecule type: protein  
A:Residues: 133,'X',135-137,'X',139-140,'X',142-144,'X',146 <BU3>  
C:Genetics:  
A:Gene: GDB:TFPI2  
A:Cross-references: GDB:354485  
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor  
C:Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-235/Product: tissue factor pathway inhibitor-2 #status predicted <MAT>  
F:36-86/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
F:96-149/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>  
F:158-208/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>  
F:36-86,45-69,61-82,96-149,106-130,122-145,158-208,167-191,183-204/Disulfide bonds: #sta

Query Match 25.2%; Score 384.5; DB 2; Length 235;  
Best Local Similarity 31.6%; Pred. No. 2.9e-24;  
Matches 78; Conservative 35; Mismatches 71; Indels 63; Gaps 7;

Qy 26 CAFKADDPCKAIMKRFNFITROCEEFYGGCEGNNRPFESLECKKMTDRDNANRII 85  
Db 36 CLPLDLYGPCRALLLRYVYDRTQSCFQFLYGGCEGNANFYTWACDDACWR----- 88

Qy 86 KTLQOEKDFCFLE---EDPGICRGYITRYFNNQTKQERFKYGGCLGNM--NNPETL 140  
Db 89 ----IEKVPKVCRLQSVDDQ--CEGSTERYFFNLSSMTCEKFPFSGGCHRNRIENRPPDE 142

Qy 141 BECKNICEGDPNGQVDNYGTQLNAVNNLSLPQSTKVPSPLEFPHGSPWCLTPADRGICRA 200  
Db 143 ATCMGFC-----APKKI-----PSFCSPKDEGLCSA 169

Qy 201 NENRYFNVSVIGKCRPFYSGCGNENFTSKOECLACKKGFQIRISKGLIKTKRKK 260  
Db 170 NVTRYFNPRTCDFTYTGCGNDNNFVSREDCKKACAKAL-----KKKKK 217

Qy 261 KQVKIA 267  
Db 218 MPKLRF 224

RESULT 8  
C89114  
protein C37C3.6a [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: C89114  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.ele  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: C89114  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1558 <STO>  
A:Cross-references: UNIPROT:Q81710; GB:chr\_V; PIDN:AAC25867.1; PID:g3294501; GSPDB:GN000  
C:Genetics:  
A:Gene: C37C3.6a  
A:Map position: 5

Query Match 23.3%; Score 355.5; DB 2; Length 1558;  
Best Local Similarity 28.8%; Pred. No. 5.2e-21;  
Matches 77; Conservative 32; Mismatches 83; Indels 75; Gaps 6;

Qy 18 PLKLMHSFCFAKDDGPKCKAIMKRFNFITROCEEFYGGCEGNNRPFESLECKKMC- 76  
Db 1263 PROSMEDICRSRODAGPCETYSDQWFFNAPFSQBCEFTYTGCGGNLNRFRSKDEQRCF 1322

Qy 77 ----TRDNANR-----IIKTLQKEP-----DFCFLEEDPG 104  
Db 1323 FVHGAQPSAAEQEAQAPAAQAPQAPGNIVSPQOSASPVVPSNSKQRDACHLNVDDQ 1382  
Qy 105 ICRGYITRYFNNOTKQERFKYGGCLGNMNFETLECKNICE-----DGPNG 153  
Db 1383 RCKGAFDSWYEVATGCVTFKYTGCGGNANRFASKQDCESLCVKPASEAASAGIDGAAG 1442  
Qy 154 FOVDNYGQLNAVNNSLTPQSTKVPSLFEFHGSPWCLTPADRGLCRANENRFYNSVIGK 213  
Db 1443 -----INSV-----CDEAKDTGPTCTNFTVTKWYNKADGT 1471  
Qy 214 CRPFKYSCGGNENFTSKQECRLACK 240  
Db 1472 CNRHYGCGQGNRNFDFNEQCKAACQ 1498  
RESULT 9  
T34395  
hypothetical protein C37C3.6b - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T34395  
R:Geisel, C.; Bradshaw, H.  
submitted to the EMBL Data Library, July 1996  
A:Description: The sequence of C. elegans cosmid C37C3.  
A:Reference number: 221518  
A:Accession: T34395  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-2167 <GBI>  
A:Cross-references: UNIPROT:O76840; EMBL:U64857; PIDN:AAC25868.1; GSPDB:GN000023; CESP:C37C3.6a  
A:Experimental source: strain Bristol N2; clone C37C3  
A:Accession: T34394  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-1555, 'SKP' <GR2>  
A:Cross-references: EMBL:U64857; PIDN:AAC25867.1; GSPDB:GN000023; CESP:C37C3.6a  
A:Experimental source: strain Bristol N2; clone C37C3  
C:Genetics:  
A:Gene: CESP:C37C3.6b; CESP:C37C3.6a  
A:Map position: 5  
A:Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556/

Query Match 23.3%; Score 355.5; DB 2; Length 2167;  
Best Local Similarity 28.8%; Pred. No. 7.4e-21;  
Matches 77; Conservative 32; Mismatches 83; Indels 75; Gaps 6;

Qy 18 PLKLMHSCAFKADGCPKAKMKRFFNIFTRQCEFIYGGCEGNQNRPFESLECKKMC- 76  
Db 1263 PRQSMEDICRSQDAGPCETYSDFWYNAFSQECETFTYGGCGGNLNRFRSKDECEQRCF 1322  
Qy 77 ----TRDNANR-----IIKTLQKEP-----DFCFLEEDPG 104  
Db 1323 FVHGAQPSAAEQEAQAPAAQAPQAPGNIVSPQOSASPVVPSNSKQRDACHLNVDDQ 1382  
Qy 105 ICRGYITRYFNNOTKQERFKYGGCLGNMNFETLECKNICE-----DGPNG 153  
Db 1383 RCKGAFDSWYEVATGCVTFKYTGCGGNANRFASKQDCESLCVKPASEAASAGIDGAAG 1442  
Qy 154 FOVDNYGQLNAVNNSLTPQSTKVPSLFEFHGSPWCLTPADRGLCRANENRFYNSVIGK 213  
Db 1443 -----INSV-----CDEAKDTGPTCTNFTVTKWYNKADGT 1471  
Qy 214 CRPFKYSCGGNENFTSKQECRLACK 240  
Db 1472 CNRHYGCGQGNRNFDFNEQCKAACQ 1498  
RESULT 10  
T26063  
hypothetical protein W01F3.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T26063  
R:Cummings, P.  
submitted to the EMBL Data Library, March 1997  
A:Reference number: 220145  
A:Accession: T26063  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-2225 <WIL>  
A:Cross-references: UNIPROT:O45881; EMBL:Z92815; PIDN:CAB07294.1; GSPDB:GN000023; CESP:W01F3  
A:Experimental source: clone W01F3  
C:Genetics:  
A:Gene: CESP:W01F3.3  
A:Map position: 5  
A:Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221/1;

Query Match 22.9%; Score 350.5; DB 2; Length 2225;  
Best Local Similarity 29.6%; Pred. No. 2e-20;  
Matches 79; Conservative 32; Mismatches 91; Indels 65; Gaps 7;

Qy 1 DSEDEBHTIITDTE-----LPPLKLMHSF-----CAFKADGQPC 35  
Db 727 DEEESEVVEEQEDGKEEPHLHVQPEVSQONTVLLGGIEDTTTDSVNRCLHPRDSGNC 786  
Qy 36 KAIMKRPFFNIFTRQCEFIYGGCEGNQNRPFESLECKKMCRTDNANRIIKTLQKEKPD 95  
Db 787 RGQFVRWFFDDKKNCDVFTYTGCGGNPFASKEECAICHKPEPT-----PSATPD 839  
Qy 96 F---CFLEEDPGICRGYITRYFYNNQTKQERFKYGGCLGNMNFETLECKNICECDGPN 152  
Db 840 PSQVCSNDVDAGECNGVFERFAPDAEQDCRAFTYGGCGGNFATWQECRSRC----- 894  
Qy 153 GFQVDNYGTQLNAVNNSLTPQSTKVPSLFEFHGSPWCLTPADRGLCRANENRFYNSVIG 212  
Db 895 -----VWAMKKS--PVAT-----CEADIEVGECAGVFSRFAFDKSGIN 929  
Qy 213 KCRPFKYSCGGNENFTSKQECRLAC 239  
Db 930 ACSFTYGGCGGNANFATLQECTNKC 956  
RESULT 11  
D88550  
protein ZC84.6 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: D88550  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/projects/C\_ele  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: D88550  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1474 <STO>  
A:Cross-references: UNIPROT:O62504; GB:chr\_III; PIDN:CAA79570.1; PID:g3881447; GSPDB:GNO  
C:Genetics:  
A:Gene: ZC84.6  
A:Map position: 3

Query Match 22.7%; Score 347; DB 2; Length 1474;  
Best Local Similarity 30.7%; Pred. No. 2.4e-20;  
Matches 86; Conservative 33; Mismatches 95; Indels 66; Gaps 10;

Qy 22 MHSFCAFKADGCPKAKMKRFFNIFTRQCEFIYGGCEGNQNRPFESLECKKMC----- 77  
Db 435 MQTICTQPLRVGNCDSRVRYWYSAATRECSFEYTCQGNNDNNFETLVDCQTFCRNAAP 494  
Qy 78 -----RDNANRIIKTLQOE-----KPDFCFLEEDPG- 104

Db 495 EPRCQGOAYKDNQKQFVTCNTNROSSCPANFECYFDGNMHGCCPTKATCTSLSPSPGK 554  
Qy 105 IC-RGYITRYFYNNOTKOCERFKYGGCLGNMNNPFTLECKNICEDGPNQFQVDNYGQL 163  
Db 555 TCGPVSFKYHNPOTQCESFEYLGCDGNSWTFASRAECENYC--GVGG--CANGGSPL 610  
Qy 164 NAVNNSLTPOSTK---VPSLFEFFHGPSW-----CLTPADRG--LCRAN- 201  
Db 611 RDSNGALQCSERDGGCFSSHECYGSLGPDWMSYRCCPTKTYICGLPFPQGGSSLCGGL 670  
Qy 202 --ENRFYNSVIGKRPKFKYGGCGNENNFSTKQECCLRAC 239  
Db 671 TVVTRYFNIYTRKCSFPFYNGCDGNPNNFASLQCNFC 710

RESULT 12  
T23573  
hypothetical protein K10D3.4 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T23573  
R:McMurray, A.  
submitted to the EMBL Data Library, June 1996  
A/Reference number: Z19762  
A/Accession: T23573  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-922 <WIL>  
A/Cross-references: UNIPROT:Q21418; EMBL:Z75545; PIDN:CAA9886.1; GSPDB:GN00019; CESP:K10D3  
A/Experimental source: clone K10D3  
C/Genetics:  
A/Gene: CESP:K10D3.4  
A/Map position: 1  
A/Introns: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2

Query Match 22.3%; Score 340; DB 2; Length 922;  
Best Local Similarity 29.0%; Pred. No. 5.5e-20;  
Matches 84; Conservative 45; Mismatches 93; Indels 68; Gaps 13;

Qy 26 CAFKADGCPKAIMKRPFFNIPTQCEFIYGGCGNRRPESLECKKMC----- 76  
Db 411 KKLPRQGNCGTYSNRWFWNAKTGNCEFIYGGCGNRRPESLECKKMC----- 470  
Qy 77 -----TRDNANRII-----KTLQOEKDPDFCFLE-----EDPGI 105  
Db 471 IQGTALTDGNGFIICGSSAASATTCPAN--HYCVYDGTTCYGCCTQAYTCSLVKSGAS 528  
Qy 106 CRGYITRYFYNNOTKOCERFKYGGCLGNMNNPFTLECKNIC--EDGPNQFQV--DNYG 160  
Db 529 CGPAVTRYDSTIRTCQTYFNGCDGNSNPFATQDCKDYCRVESCPDGGVKEQNGA 588  
Qy 161 TQLNAVNS-----LTPQSTKVPSLFEFHG---PS---WCLTPADRG--LCRAN-NRFY 206  
Db 589 ARACCTNRQCPSTHYCTPVTWTGTVYQTKSLCPSKFNVCQRPDRVGRCSSTRISRWY 648  
Qy 207 YNSVIGKRPKFKYGGCGNENNFSTKQEC-----LRACKGFIORISKGG 251  
Db 649 FNADSKTCQTEFYNGCGNRRNRFASQSKQNYCLSEACPPTGV--VAKDG 696

RESULT 13  
H88380  
protein T22F7.3 [imported] - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C/Accession: H88380  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
A/Reference number: A75000; MUID:99069613; PMID:9851916  
A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.ele  
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A/Accession: H88380

A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1522 <STO>  
A/Cross-references: GB:chr\_III; PIDN:AAA20672.1; PID:g529714; GSPDB:GN00021; CESP:T22F7.  
A/Note: highly similar to ZC84.1  
C/Genetics:  
A/Gene: T22F7.3  
A/Map position: 3

Query Match 21.9%; Score 334.5; DB 2; Length 1522;  
Best Local Similarity 28.2%; Pred. No. 2.7e-19;  
Matches 90; Conservative 40; Mismatches 90; Indels 99; Gaps 14;

Qy 24 SFCAFKADGCPKAIMKRPFFNIPTQCEFIYGGCGNRRPESLECKKMCCT----- 77  
Db 531 SLCTQPKELGDCISAVRYWYNATRCSEMFOYTGCGNDNNFNTLMACQCKRGHVEP 590  
Qy 78 -----RDNANRIIITLQOEKPD-----FCLEEDPGI-C 106  
Db 591 KQHGAFRDRNGNFQCSDKQNGKPCPVNVVCSFDGTTGCGCTKATCTSLNPKGVQC 650  
Qy 107 ---RGYITRYFYNNOTKOCERFKYGGCLGNMNNPFTLECKNICEDG--PNGFQVDNYGT 161  
Db 651 GSGRSY--RYFNSNKQSCSFQYEGCDGNANFLTSEDCHQYGVGCGPNG-----GM 702  
Qy 162 QL--NAVNSLTPOSTK-VPSLFEFFHGPSWCLT-----PADRGILC----- 198  
Db 703 PLRDEATKPMSCSEKQSCPSSTHE-----CLTTPVNHVGSRCCTPKQHILCSQPQGN 756  
Qy 199 ---RANRFRFYNSVIGKRPKFKYGGCGNENNFSTKQECCLRACKGFIORISKGLIKT 255  
Db 757 HCSKISVGRFYFNIPTRECATFYNGCGNGLNPFATQSECNFCS-----SAGCAVG- 808  
Qy 256 KRREKKQKVXIAYEEIFVK 274  
Db 809 -----EVAYKDVNTK 818

RESULT 14  
E88550  
Protein ZC84.1 [imported] - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C/Accession: E88550  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
A/Reference number: A75000; MUID:99069613; PMID:9851916  
A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.ele  
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A/Accession: E88550  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1416 <STO>  
A/Cross-references: UNIPROT:Q03610; GB:chr\_III; PIDN:CAA9569.1; PID:g3881446; GSPDB:GN0  
A/Note: similar to Serine protease inhibitor, Kunitz type  
C/Genetics:  
A/Gene: ZC84.1  
A/Map position: 3

Query Match 21.8%; Score 332.5; DB 2; Length 1416;  
Best Local Similarity 31.6%; Pred. No. 3.6e-19;  
Matches 87; Conservative 29; Mismatches 92; Indels 67; Gaps 11;

Qy 24 SFCAFKADGCPKAIMKRPFFNIPTQCEFIYGGCGNRRPESLECKKMCCTRDNANR 83  
Db 432 TICAPLRIGDCTENVKRYWYNATRCQMFYTGCGNDNNFDSIMDCNFC--KNAIP 489  
Qy 84 IIKTLQOEKPDF-----CFLEEDPGI-C- 106  
Db 490 EPKICIQGAYKDMFGNPFVTCNSGMGCPANVECYFDGSGWCCPCTKATCTSLNDSGIQCG 549  
Qy 107 RGYITRYFYNNOTKOCERFKYGGCLGNMNNPFTLECKNICEDG--PNGFQVDNYGTQLN 164

```
Db      550 AGSTFKYYNQTCNCSFQYNGCDGNSNNFANRDACESYCSVGGCPNG-----GTPLR 603
Qy      165 AVNNSLT---PQSTKVP-----SLFEFHGPS---WCLTPADRGGL-CRAN-ENR 204
Db      604 DHSGWMVVCQAQQTSCPDSCHECIPVLVGNLSLNRCCPTRAYMCGLPPOQGTCCGANYVQR 663
Qy      205 FYNRSVICKCRPFKYSGCGGNNFTSKOECLRAC 239
Db      664 YFNIIVTSQCTSFQFGGCDGNANFNLIQQRNFC 698
```

## RESULT 15

```
S28291
hypochemical protein ZC84.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S28291
R:Thomas, K.
submitted to the EMBL Data Library, December 1992
A:Reference number: S28285
A:Accession: S28291
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2844 <THO>
A:Cross-references: UNIPROT:Q03610; EMBL:Z19157
C:Genetics:
A:Introns: 14/1; 32/3; 57/1; 192/3; 277/1; 398/1; 439/1; 474/1; 497/1; 813/1; 1135/1; 12
493/1; 2555/1; 2720/1; 2739/3; 2819/1
F:220-274/Domain: animal Kunitz-type proteinase inhibitor homology <BPI1>
F:343-395/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>
F:442-492/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>
F:546-598/Domain: animal Kunitz-type proteinase inhibitor homology <BPI4>
F:654-706/Domain: animal Kunitz-type proteinase inhibitor homology <BPI5>
F:1662-1716/Domain: animal Kunitz-type proteinase inhibitor homology <BPI6>
F:1787-1839/Domain: animal Kunitz-type proteinase inhibitor homology <BPI7>
F:1845-1895/Domain: animal Kunitz-type proteinase inhibitor homology <BPI8>
F:1952-2004/Domain: animal Kunitz-type proteinase inhibitor homology <BPI9>
F:2097-2152/Domain: animal Kunitz-type proteinase inhibitor homology <BPI10>
```

```
Query Match      21.8%; Score 332.5; DB 2; Length 2844;
Best Local Similarity 31.6%; Pred. No. 7.6e-19;
Matches 87; Conservative 29; Mismatches 92; Indels 67; Gaps 11;
Qy      24 SFCAFKADGPKCKALMKRFFNIFTRQCEEFYGGCEGNQNRFSLECKKMCRTDNR 83
Db      440 TICAQPLRIGDCTENVKRYWYNARTQCMPFYTCQGNNDNFDSDIMDCQNF--KNAIP 497
Qy      84 IIKTTLQEKPDF-----CFLIEDPGI-C- 106
Db      498 EPKCIQQAQYKDMFGNFVTCNGMGCPANYCYFDGQWGCGCPTKAFCTSLNTDSGIQCG 557
Qy      107 RGYITRYFYNNQTKOCERFKYGGCLGNMNFETLECKNICEDG--PNGFQVDNYGTOLN 164
Db      558 AGSTFKYYNQTCNCSFQYNGCDGNSNNFANRDACESYCSVGGCPNG-----GTPLR 611
Qy      165 AVNNSLT---PQSTKVP-----SLFEFHGPS---WCLTPADRGGL-CRAN-ENR 204
Db      612 DHSGWMVVCQAQQTSCPDSCHECIPVLVGNLSLNRCCPTRAYMCGLPPOQGTCCGANYVQR 671
Qy      205 FYNRSVICKCRPFKYSGCGGNNFTSKOECLRAC 239
Db      672 YFNIIVTSQCTSFQFGGCDGNANFNLIQQRNFC 706
```

Search completed: April 16, 2005, 03:28:47  
Job time : 46 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2005, 03:21:23 ; Search time 43 Seconds  
(without alignments)  
479.143 Million cell updates/sec

Title: US-10-753-079-1  
Perfect score: 1528  
Sequence: 1 DSEDEHTIITDELPLK.....RKRKKQKVIAIEIFVKQM 276

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pap:\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pap:\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pap:\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1528	100.0	276	2	US-08-796-850-1
2	1528	100.0	276	4	US-09-766-778-1
3	1528	100.0	277	1	US-07-844-297-1
4	1528	100.0	304	1	US-08-026-145-2
5	1528	100.0	304	1	US-08-446-646-9
6	1528	100.0	304	1	US-08-676-124-1
7	1528	100.0	304	2	US-09-136-012A-18
8	1528	100.0	304	3	US-08-676-124-1
9	1528	100.0	304	3	US-08-208-264A-25
10	1528	100.0	304	3	US-09-414-878-1
11	1528	100.0	304	3	US-09-240-136-1
12	1528	100.0	304	3	US-09-421-097-25
13	1528	100.0	304	4	US-09-638-770A-1
14	1528	100.0	304	4	US-09-054-272-16
15	1528	100.0	304	6	5466783-2
16	1528	100.0	304	6	5466783-2
17	1528	100.0	352	3	US-08-854-764-2
18	1528	100.0	352	5	PCT-US95-09377-2
19	1528	100.0	381	4	US-09-949-016-7400
20	1525	99.8	276	1	US-08-437-841-9
21	1525	99.8	276	1	US-08-286-521-9
22	1525	99.8	276	1	US-08-436-175-9
23	1525	99.8	276	3	US-08-854-764-3
24	1525	99.8	276	3	US-08-943-682-9
25	1525	99.8	276	4	US-09-741-106-9
26	1525	99.8	276	5	PCT-US95-09377-3
27	1525	99.8	276	5	PCT-US95-09464-9

28	1522	99.6	304	3	US-09-054-782-2	Sequence 2, Appli
29	1522	99.6	304	4	US-09-627-676-2	Sequence 2, Appli
30	1522	99.6	304	4	US-10-377-876-2	Sequence 2, Appli
31	1521	99.5	276	1	US-07-828-920A-1	Sequence 1, Appli
32	1517	99.3	304	4	US-09-763-565-2	Sequence 2, Appli
33	1507	98.6	304	4	US-09-763-565-4	Sequence 4, Appli
34	1447.5	94.7	291	4	US-10-000-489-48	Sequence 48, Appli
35	1444.5	94.5	291	4	US-10-000-489-52	Sequence 52, Appli
36	1180.5	77.3	213	6	5466783-25	Patent No. 5466783
37	1180.5	77.3	213	6	5466783-25	Patent No. 5466783
38	900	58.9	189	1	US-07-828-920A-7	Sequence 7, Appli
39	897	58.7	161	1	US-08-437-841-19	Sequence 19, Appli
40	897	58.7	161	1	US-08-286-521-19	Sequence 19, Appli
41	897	58.7	161	1	US-08-436-175-19	Sequence 19, Appli
42	897	58.7	161	3	US-08-943-682-19	Sequence 19, Appli
43	897	58.7	161	4	US-09-741-106-19	Sequence 19, Appli
44	897	58.7	161	5	PCT-US95-09464-19	Sequence 19, Appli
45	834	54.6	183	1	US-07-828-920A-5	Sequence 5, Appli

## ALIGNMENTS

RESULT 1  
US-08-796-850-1  
; Sequence 1, Application US/08796850  
; Patent No. 5981471  
; GENERAL INFORMATION:  
; APPLICANT: Papathanassiou, Adonia E  
; APPLICANT: Green, Shawn J.  
; TITLE OF INVENTION: Compositions and Methods for Inhibiting  
; TITLE OF INVENTION: Cellular Proliferation  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: U.S.A.  
; ZIP: 30303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/796,850  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Greene, Jamie L.  
; REGISTRATION NUMBER: 32,467  
; REFERENCE/DOCKET NUMBER: 05213-0290  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 818-3700  
; TELEFAX: (404) 818-3799  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 276 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: Active-site  
; LOCATION: 2..3  
; OTHER INFORMATION: /note= "Site of partial phosphorylation"

FEATURE:  
NAME/KEY: Active-site  
LOCATION: 117..118  
OTHER INFORMATION: /note= "Potential site for N-linked  
OTHER INFORMATION: glycosylation"  
FEATURE:  
NAME/KEY: Active-site  
LOCATION: 167..168  
OTHER INFORMATION: /note= "Potential site for N-linked  
OTHER INFORMATION: glycosylation"  
FEATURE:  
NAME/KEY: Active-site  
LOCATION: 228..229  
OTHER INFORMATION: /note= "Potential site for N-linked  
OTHER INFORMATION: glycosylation"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 26..76  
OTHER INFORMATION: /label= Kunitz-1  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 97..147  
OTHER INFORMATION: /label= Kunitz-2  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 189..239  
OTHER INFORMATION: /label= Kunitz-3

US-08-796-850-1

Query Match 100.0%; Score 1528; DB 2; Length 276;  
Best Local Similarity 100.0%; Pred. No. 1.1e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSEDEEHTIITDLPPLKLMHSCAFKADGPKAKMKRFFNFTRQCEEFYGGCE 60  
DB 1 DSEDEEHTIITDLPPLKLMHSCAFKADGPKAKMKRFFNFTRQCEEFYGGCE 60  
QY 61 GNQRFESLECKKCTRDNANRIKTTLOQEKDPFCFLEEDPGICRGYITRYFYNNOTK 120  
DB 61 GNQRFESLECKKCTRDNANRIKTTLOQEKDPFCFLEEDPGICRGYITRYFYNNOTK 120  
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QY 181 FEFHGPSWCLTPADRGLCRANERNRYNSVIGKCRPFYSGCGNENFTSKQECCLACK 240  
DB 181 FEFHGPSWCLTPADRGLCRANERNRYNSVIGKCRPFYSGCGNENFTSKQECCLACK 240  
QY 241 KGFIQIRISKGLIKTKRKRKQKVIAEIEIFVKNM 276  
DB 241 KGFIQIRISKGLIKTKRKRKQKVIAEIEIFVKNM 276

RESULT 2  
US-09-766-778-1  
Sequence 1, Application US/09766778  
Patent No. 6734163  
GENERAL INFORMATION:  
APPLICANT: Papathanassiou, Adonia E  
Green, Shawn J.  
TITLE OF INVENTION: Compositions and Methods for Inhibiting  
Cellular Proliferation  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.A.  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/766,778  
FILING DATE: 22-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/227,955  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Greene, Jamie L.  
REGISTRATION NUMBER: 32,467  
REFERENCE/DOCKET NUMBER: 05213-0290  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 818-3700  
TELEFAX: (404) 818-3799  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 276 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: Active-site  
LOCATION: 2..3  
OTHER INFORMATION: /note= "Site of partial  
phosphorylation"  
FEATURE:  
NAME/KEY: Active-site  
LOCATION: 117..118  
OTHER INFORMATION: /note= "Potential site for N-linked  
glycosylation"  
FEATURE:  
NAME/KEY: Active-site  
LOCATION: 167..168  
OTHER INFORMATION: /note= "Potential site for N-linked  
glycosylation"  
FEATURE:  
NAME/KEY: Active-site  
LOCATION: 228..229  
OTHER INFORMATION: /note= "Potential site for N-linked  
glycosylation"  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 26..76  
OTHER INFORMATION: /label= Kunitz-1  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 97..147  
OTHER INFORMATION: /label= Kunitz-2  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 189..239  
OTHER INFORMATION: /label= Kunitz-3  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-766-778-1

Query Match 100.0%; Score 1528; DB 4; Length 276;  
Best Local Similarity 100.0%; Pred. No. 1.1e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSEDEEHTIITDLPPLKLMHSCAFKADGPKAKMKRFFNFTRQCEEFYGGCE 60  
DB 1 DSEDEEHTIITDLPPLKLMHSCAFKADGPKAKMKRFFNFTRQCEEFYGGCE 60  
QY 61 GNQRFESLECKKCTRDNANRIKTTLOQEKDPFCFLEEDPGICRGYITRYFYNNOTK 120

Db 61 GNQRFESLECKKCMCTDNNR1IKTTLQEKDPFCFLEEDPGICRGYITRYFNNQTK 120  
QY 121 QCFERYGGCLGNMNFETLECKNICEDGPNQFVDNYGTQLNANNVNSLTPOSTKVPSSL 180  
Db 121 QCFERYGGCLGNMNFETLECKNICEDGPNQFVDNYGTQLNANNVNSLTPOSTKVPSSL 180  
QY 181 FEFHGPSWCLTPADRGCLCRANENRFFYNVSGKCRPFKYSGCGNENFTSKQECRLACK 240  
Db 181 FEFHGPSWCLTPADRGCLCRANENRFFYNVSGKCRPFKYSGCGNENFTSKQECRLACK 240  
QY 241 KGFIORISKGGLIKTKRKRKQORVIAEIEIFVKNM 276  
Db 241 KGFIORISKGGLIKTKRKRKQORVIAEIEIFVKNM 276

RESULT 3  
US-07-844-297-1  
; Sequence 1, Application US/07844297  
; Patent No. 5212091  
; GENERAL INFORMATION:  
; APPLICANT: Diaz-Collier, Judy A.  
; APPLICANT: Gustafson, Mark E.  
; APPLICANT: Wun, Tze-Chien  
; TITLE OF INVENTION: Method of Producing Tissue Factor  
; TITLE OF INVENTION: Pathway Inhibitor  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG  
; STREET: 800 N. Lindbergh Blvd.  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 63167

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/844,297  
; FILING DATE: 19920302  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyer, Scott J.  
; REGISTRATION NUMBER: 25,275  
; REFERENCE/DOCKET NUMBER: 07-21(819)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)694-3117  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 277 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-844-297-1

Query Match 100.0%; Score 1528; DB 1; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1.1e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 GNQRFESLECKKCMCTDNNR1IKTTLQEKDPFCFLEEDPGICRGYITRYFNNQTK 120  
Db 62 GNQRFESLECKKCMCTDNNR1IKTTLQEKDPFCFLEEDPGICRGYITRYFNNQTK 121  
QY 121 QCFERYGGCLGNMNFETLECKNICEDGPNQFVDNYGTQLNANNVNSLTPOSTKVPSSL 180  
Db 122 QCFERYGGCLGNMNFETLECKNICEDGPNQFVDNYGTQLNANNVNSLTPOSTKVPSSL 181

QY 181 FEFHGPSWCLTPADRGCLCRANENRFFYNVSGKCRPFKYSGCGNENFTSKQECRLACK 240  
Db 182 FEFHGPSWCLTPADRGCLCRANENRFFYNVSGKCRPFKYSGCGNENFTSKQECRLACK 241  
QY 241 KGFIORISKGGLIKTKRKRKQORVIAEIEIFVKNM 276  
Db 242 KGFIORISKGGLIKTKRKRKQORVIAEIEIFVKNM 277

RESULT 4  
US-08-026-145-2  
; Sequence 2, Application US/08026145  
; Patent No. 5378614  
; GENERAL INFORMATION:  
; APPLICANT: Petersen, Jens G. Liteke  
; APPLICANT: No. 5378614dfang, Ole Juul  
; TITLE OF INVENTION: Method for Making TFPI Analogues  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 53786140 No. 5378614disk of No. 5378614th America, Inc.  
; STREET: 405 Lexington Avenue, Suite 6200  
; CITY: New York  
; STATE: N. Y.  
; COUNTRY: United States of America  
; ZIP: 10174-6201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/026,145  
; FILING DATE: 19930302  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/828,920  
; FILING DATE: 27-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/DK/90/00212  
; FILING DATE: 17-AUG-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 4080/89  
; FILING DATE: 18-AUG-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Agriis, Cheryl H.  
; REGISTRATION NUMBER: 34086  
; REFERENCE/DOCKET NUMBER: 3321.214-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 867 0123  
; TELEFAX: 212 867 0298  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-026-145-2

Query Match 100.0%; Score 1528; DB 1; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKCAIMKRPFFNIFTRQCEEFYGGCE 60  
Db 29 DSEDEEHTIITDTELPPLKLMHSFCAPKADGPKCAIMKRPFFNIFTRQCEEFYGGCE 88  
QY 61 GNQRFESLECKKCMCTDNNR1IKTTLQEKDPFCFLEEDPGICRGYITRYFNNQTK 120  
Db 89 GNQRFESLECKKCMCTDNNR1IKTTLQEKDPFCFLEEDPGICRGYITRYFNNQTK 148  
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Db 149 QCFERYGGCLGNMNFETLECKNICEDGPNQFVDNYGTQLNANNVNSLTPOSTKVPSSL 208

QY 181 FEHFGPSWCLTPADRGGLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKOECLACK 240  
Db 209 FEHFGPSWCLTPADRGGLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKOECLACK 268  
QY 241 KGFIQISKGLIKTKRRKKQKQKVIAYEEIFVKNM 276  
Db 269 KGFIQISKGLIKTKRRKKQKQKVIAYEEIFVKNM 304

## RESULT 5

US-08-446-646-9  
; Sequence 9, Application US/08446646  
; Patent No. 5726038  
; GENERAL INFORMATION:  
; APPLICANT: Christiansen, Lars  
; APPLICANT: Petersen, Jens G.  
; TITLE OF INVENTION: A DNA Construct Encoding the YAP3 Signal  
; TITLE OF INVENTION: Peptide  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 57260380 No. 5726038disk of No. 5726038th America, Inc.  
; STREET: 405 Lexington Avenue, 64th Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10174-6401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,646  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lambiris, Elias J.  
; REGISTRATION NUMBER: 33,728  
; REFERENCE/DOCKET NUMBER: 3987.204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-878-9655  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-446-646-9

Query Match 100.0%; Score 1528; DB 1; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSEDEEHTIITDTEPLPLKMHSCAFKADGPKAIWKPFNIFTRQCEEFYGGCE 60  
Db 29 DSEDEEHTIITDTEPLPLKMHSCAFKADGPKAIWKPFNIFTRQCEEFYGGCE 88  
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Db 89 GNQNFESLECKKMCCTRDNANRIITLQOEKPDFCFLEEDPGICRGYITRYFYNNQTK 148  
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Db 269 KGFIQISKGLIKTKRRKKQKQKVIAYEEIFVKNM 304

Db 269 KGFIQISKGLIKTKRRKKQKQKVIAYEEIFVKNM 304

## RESULT 6

US-08-676-125A-18  
; Sequence 18, Application US/08676125A  
; Patent No. 5795865  
; GENERAL INFORMATION:  
; APPLICANT: MARKLAND, William  
; APPLICANT: LADNER, Robert Charles  
; TITLE OF INVENTION: KALLIKREIN-INHIBITING "KUNITZ DOMAIN" PROTEINS AND ANALOGUES  
; NUMBER OF SEQUENCES: 70  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yankwich & Associates  
; STREET: 130 Bishop Allen Drive, fifth floor  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: United States of America  
; ZIP: 02139  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word for Windows 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/676,125A  
; FILING DATE: 25 September 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/00299  
; FILING DATE: 11 January 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/179,964  
; FILING DATE: 11 January 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/208,264  
; FILING DATE: 10 March 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YANKWICH, Leon R.  
; REGISTRATION NUMBER: 30,237  
; REFERENCE/DOCKET NUMBER: DYX-006.2P US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 491-4343  
; TELEFAX: (617) 491-8801  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-676-125A-18

Query Match 100.0%; Score 1528; DB 1; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSEDEEHTIITDTEPLPLKMHSCAFKADGPKAIWKPFNIFTRQCEEFYGGCE 60  
Db 29 DSEDEEHTIITDTEPLPLKMHSCAFKADGPKAIWKPFNIFTRQCEEFYGGCE 88  
QY 61 GNQNFESLECKKMCCTRDNANRIITLQOEKPDFCFLEEDPGICRGYITRYFYNNQTK 120  
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QY 121 QCERFKYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNANNSLTPQSTKVPSL 180  
Db 149 QCERFKYGGCLGNMNFETLECKNICEDGPNQFQVDNYGTQLNANNSLTPQSTKVPSL 208  
QY 181 FEHFGPSWCLTPADRGGLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKOECLACK 240  
Db 209 FEHFGPSWCLTPADRGGLCRANENRFFYNSVIGKCRPFKYSGCGNENFTSKOECLACK 268

Oy 241 KGFIORISKGLIKTKRKRKQVVKIAYEIEFVKNM 276  
Db 269 KGFIORISKGLIKTKRKRKQVVKIAYEIEFVKNM 304

## RESULT 7

US-09-136-012A-18  
; Sequence 18, Application US/09136012A  
; Patent No. 5994125  
; GENERAL INFORMATION:  
; APPLICANT: DYAX CORP  
; APPLICANT: MARKLAND, William  
; APPLICANT: LADNER, Robert Charles  
; TITLE OF INVENTION: KALLIKREIN-INHIBITING "KUNITZ DOMAIN" PROTEINS  
; TITLE OF INVENTION: AND ANALOGUES THEREOF  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yankwich & Associates  
; STREET: 130 Bishop Allen Drive, fifth floor  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: United States of America  
; ZIP: 02139  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5-inch diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Microsoft Windows 98  
; SOFTWARE: Microsoft Word 97 SR-1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/136.012A  
; FILING DATE: 17-August-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/676,125  
; FILING DATE: 25-September-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/00299  
; FILING DATE: 11-January-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/208,264  
; FILING DATE: 10-March-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/179,964  
; FILING DATE: 11-January-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YANKWICH, Leon R.  
; REGISTRATION NUMBER: 30,237  
; NAME: ZWICKER, Kenneth P.  
; REGISTRATION NUMBER: 43,310  
; REFERENCE/DOCKET NUMBER: DYX-006.2P US-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 491-4343  
; TELEFAX: (617) 491-8801  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-136-012A-18

Query Match 100.0%; Score 1528; DB 2; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 DSEDEEHTIITDELPLKLMHSFCAPKADGPKCAIMKFFNIFTRQCEEFYGGCE 60  
Db 29 DSEDEEHTIITDELPLKLMHSFCAPKADGPKCAIMKFFNIFTRQCEEFYGGCE 88  
Oy 61 GQNRFSLECKKMCCTRDNANRIKTTLOQEKDPDFCFLEEDPGICRGYITRYFNNQTK 120  
Db 89 GQNRFSLECKKMCCTRDNANRIKTTLOQEKDPDFCFLEEDPGICRGYITRYFNNQTK 148

Oy 121 QCERFKYGGCLGNMNFETLEECKNICEDGNGFQVDNYGTOLNANNSLTPQSTKVPSL 180  
Db 149 QCERFKYGGCLGNMNFETLEECKNICEDGNGFQVDNYGTOLNANNSLTPQSTKVPSL 208  
Oy 181 FEFHGPSWCLTPADRGLCRANENFYNSVIGKCRPFKYSGCGGNNNFTSKQECCLACK 240  
Db 209 FEFHGPSWCLTPADRGLCRANENFYNSVIGKCRPFKYSGCGGNNNFTSKQECCLACK 268  
Oy 241 KGFIORISKGLIKTKRKRKQVVKIAYEIEFVKNM 276  
Db 269 KGFIORISKGLIKTKRKRKQVVKIAYEIEFVKNM 304

## RESULT 8

US-08-676-124-1  
; Sequence 1, Application US/08676124  
; Patent No. 6010880  
; GENERAL INFORMATION:  
; APPLICANT: MARKLAND, William  
; APPLICANT: LADNER, Robert Charles  
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED  
; TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: United States of America  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/676,124  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/00298  
; FILING DATE: 11-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/179,658  
; FILING DATE: 11-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/208,265  
; FILING DATE: 10-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, IVER P.  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: MARKLAND=3B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-676-124-1

Query Match 100.0%; Score 1528; DB 3; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 DSEDEEHTIITDELPLKLMHSFCAPKADGPKCAIMKFFNIFTRQCEEFYGGCE 60  
Db 29 DSEDEEHTIITDELPLKLMHSFCAPKADGPKCAIMKFFNIFTRQCEEFYGGCE 88  
Oy 61 GQNRFSLECKKMCCTRDNANRIKTTLOQEKDPDFCFLEEDPGICRGYITRYFNNQTK 120

Db 89 GQNRFSLECKKCMCTRDNANRIKTTIQEKPDPFCFLEEDPGICRGYITRYFNNQTK 148  
QY 121 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTOLNAVNNSLTPQSTKVPSL 180  
Db 149 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTOLNAVNNSLTPQSTKVPSL 208  
QY 181 FEFHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSGCGGNNFTSKQECCLACK 240  
Db 209 FEFHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSGCGGNNFTSKQECCLACK 268  
QY 241 KGFIORISKGLIKTKRKKQKQVIAVEEIFVKNM 276  
Db 269 KGFIORISKGLIKTKRKKQKQVIAVEEIFVKNM 304

## RESULT 9

US-08-208-264A-25  
; Sequence 25, Application US/08208264A  
; Patent No. 6057287

; GENERAL INFORMATION:  
; APPLICANT: MARKLAND, William  
; APPLICANT: LADNER, Robert C.  
; TITLE OF INVENTION: KALLIKREIN-BINDING "KUNITZ DOMAIN"  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yankwich & Associates  
; STREET: 130 Bishop Allen Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02139

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5-inch diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Microsoft Windows 95  
; SOFTWARE: Microsoft Word 97  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/208,264A  
; FILING DATE: 10-MAR-1994  
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/179,964  
; FILING DATE: 11-JAN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Leon R. Yankwich  
; REGISTRATION NUMBER: 30,237  
; REFERENCE/DOCKET NUMBER: DYX-006.1 US

; TELEPHONE: 617-491-4343  
; TELEFAX: 617-491-8801  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-208-264A-25

Query Match 100.0%; Score 1528; DB 3; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTITDTLPLKLMHSCAFKADGPKCKALMKRFFNIFTRQCEEFYGGCE 60  
Db 29 DSEDEEHTITDTLPLKLMHSCAFKADGPKCKALMKRFFNIFTRQCEEFYGGCE 88  
QY 61 GQNRFSLECKKCMCTRDNANRIKTTIQEKPDPFCFLEEDPGICRGYITRYFNNQTK 120  
Db 89 GQNRFSLECKKCMCTRDNANRIKTTIQEKPDPFCFLEEDPGICRGYITRYFNNQTK 148

QY 121 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTOLNAVNNSLTPQSTKVPSL 180  
Db 149 QCERFKYGGCLGNMNNFETLECKNICEDGPNQFQVDNYGTOLNAVNNSLTPQSTKVPSL 208  
QY 181 FEFHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSGCGGNNFTSKQECCLACK 240  
Db 209 FEFHGPSWCLTPADRGCLCRANENFYNSVIGKCRPFKYSGCGGNNFTSKQECCLACK 268  
QY 241 KGFIORISKGLIKTKRKKQKQVIAVEEIFVKNM 276  
Db 269 KGFIORISKGLIKTKRKKQKQVIAVEEIFVKNM 304

## RESULT 10

US-09-414-878-1  
; Sequence 1, Application US/09414878  
; Patent No. 6071723

; GENERAL INFORMATION:  
; APPLICANT: DYAX CORP  
; APPLICANT: MARKLAND, William  
; APPLICANT: LADNER, Robert C.  
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived  
; NUMBER OF SEQUENCES: 139  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yankwich & Associates  
; STREET: 130 Bishop Allen Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02139

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5-inch diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Microsoft Windows 98  
; SOFTWARE: Microsoft Word 97 SR-1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/414,878  
; FILING DATE: (currently herewith)  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/240,136  
; FILING DATE: 29-JAN-1999  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/676,124  
; FILING DATE: 07-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/00298  
; FILING DATE: 11-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/208,265  
; FILING DATE: 10-MAR-1994  
; APPLICATION NUMBER: 08/179,685  
; FILING DATE: 11-JAN-1994

; ATTORNEY/AGENT INFORMATION:  
; NAME: YANKWICH, Leon R  
; REGISTRATION NUMBER: 30,237  
; NAME: ZWICKER, Kenneth P  
; REGISTRATION NUMBER: 43,310  
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-491-4343  
; TELEFAX: 617-491-8801  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-414-878-1

Query Match 100.0%; Score 1528; DB 3; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145; Indels 0; Gaps 0;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSEDEEHTIITDTELPPLKLMHSCAFKADGPKCKAIIKMFNFTFQCEEFYGGCE 60  
DB 29 DSEDEEHTIITDTELPPLKLMHSCAFKADGPKCKAIIKMFNFTFQCEEFYGGCE 88  
QY 61 GNQRFESLECKKCMCTRDNANRII KTTLOQKPDPCFLEEDPGICRGYITRYFYNNQTK 120  
DB 89 GNQRFESLECKKCMCTRDNANRII KTTLOQKPDPCFLEEDPGICRGYITRYFYNNQTK 148  
QY 121 QCERFKYGGCLGNMNNFETLECKNICEDGPGNFQVDNYGTOLNANNSLTPQSTKVPSL 180  
DB 149 QCERFKYGGCLGNMNNFETLECKNICEDGPGNFQVDNYGTOLNANNSLTPQSTKVPSL 208  
QY 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKOECLRACK 240  
DB 209 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKOECLRACK 268  
QY 241 KGFQIRISKGGLIKTKRKRKQKVIAEIEIFVKM 276  
DB 269 KGFQIRISKGGLIKTKRKRKQKVIAEIEIFVKM 304

## RESULT 11

US-09-240-136-1  
; Sequence 1, Application US/09240136  
; Patent No. 6103499  
; GENERAL INFORMATION:  
; APPLICANT: DYAX CORP  
; APPLICANT: MARKLAND, William  
; APPLICANT: LADNER, Robert C  
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived  
; TITLE OF INVENTION: From The Kunitz Domains  
; NUMBER OF SEQUENCES: 139  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yankwich & Associates  
; STREET: 130 Bishop Allen Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02139  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5-inch diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Microsoft Windows 98  
; SOFTWARE: Microsoft Word 97 SR-1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/240,136  
; FILING DATE: (concurrently herewith)  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/676,124  
; FILING DATE: 07-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/00298  
; FILING DATE: 11-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/208,265  
; FILING DATE: 10-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/179,685  
; FILING DATE: 11-JAN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YANKWICH, Leon R  
; REGISTRATION NUMBER: 30,237  
; NAME: ZWICKER, Kenneth P  
; REGISTRATION NUMBER: 43,310  
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-491-4343  
; TELEFAX: 617-491-8801

## ; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 304 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-240-136-1  
Query Match 100.0%; Score 1528; DB 3; Length 304;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSEDEEHTIITDTELPPLKLMHSCAFKADGPKCKAIIKMFNFTFQCEEFYGGCE 60  
DB 29 DSEDEEHTIITDTELPPLKLMHSCAFKADGPKCKAIIKMFNFTFQCEEFYGGCE 88  
QY 61 GNQRFESLECKKCMCTRDNANRII KTTLOQKPDPCFLEEDPGICRGYITRYFYNNQTK 120  
DB 89 GNQRFESLECKKCMCTRDNANRII KTTLOQKPDPCFLEEDPGICRGYITRYFYNNQTK 148  
QY 121 QCERFKYGGCLGNMNNFETLECKNICEDGPGNFQVDNYGTOLNANNSLTPQSTKVPSL 180  
DB 149 QCERFKYGGCLGNMNNFETLECKNICEDGPGNFQVDNYGTOLNANNSLTPQSTKVPSL 208  
QY 181 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKOECLRACK 240  
DB 209 FEFHGPSWCLTPADRGCLCRANENRFYNSVIGKCRPFKYSGCGGNENFTSKOECLRACK 268  
QY 241 KGFQIRISKGGLIKTKRKRKQKVIAEIEIFVKM 276  
DB 269 KGFQIRISKGGLIKTKRKRKQKVIAEIEIFVKM 304

## RESULT 12

US-09-421-097-25  
; Sequence 25, Application US/09421097  
; Patent No. 6333402  
; GENERAL INFORMATION:  
; APPLICANT: MARKLAND, William  
; APPLICANT: LADNER, Robert C  
; TITLE OF INVENTION: KALLIKREIN-BINDING "KUNITZ DOMAIN"  
; TITLE OF INVENTION: PROTEINS AND ANALOGUES THEREOF  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yankwich & Associates  
; STREET: 130 Bishop Allen Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02139  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5-inch diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Microsoft Windows 98  
; SOFTWARE: Microsoft Word 97  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/421,097  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/208,264  
; FILING DATE: 10-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/179,964  
; FILING DATE: 11-JAN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Leon R. Yankwich  
; REGISTRATION NUMBER: 30,237  
; REFERENCE/DOCKET NUMBER: DYX-006.1 US-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-491-4343  
; TELEFAX: 617-491-8801

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